

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 13:28:23 ; Search time 1452.41 Seconds

(without alignments)  
10479.665 Million cell updates/sec

Title: US-09-852-261-5

Perfect score: 523

Sequence: 1 ggaacggagagcgtcgtcg...aaatcaccaagtaaacattc 523

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
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41: em-htg-mus: \*  
42: em-htg-other: \*

Score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	100.0	523	6	AX147746
2	523	100.0	523	6	AX300783
3	467.4	89.4	517	6	AX147742
4	467.4	89.4	517	6	AX300779
5	409	78.2	471	6	AX147754
6	409	78.2	471	6	AX300791
7	364.8	63.8	1536	10	BC012409
8	361.6	63.1	1298	10	RN1612
9	361.6	63.1	958	10	RN1612
10	358.4	68.5	710	10	RN1612
11	356.8	68.2	539	6	AX147744
12	356.8	68.2	539	6	AX300781
13	349.4	66.8	651	10	MM1612
14	336	64.2	432	4	AF022961
15	334.4	63.9	7260	6	AX375028
16	334.4	63.9	7260	6	AX411095
17	334.4	63.9	7260	6	HS1612
18	332.8	63.6	666	6	A29119
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21	332.4	63.6	616	9	HS1612
22	331.2	63.3	620	6	I08370
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27	286.2	54.7	888	4	EC085272
28	281.8	53.9	978	4	COTGFI1
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30	280.2	53.6	1264	4	BT1612
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35	275.2	52.6	730	9	HS1612
36	275.2	52.6	1094	9	HUMGFI1
37	275.2	52.6	1136	6	E01349
38	273.6	52.3	612	9	HUMGFI1
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45	263.6	50.4	1346	10	RN1612

#### ALIGNMENTS

RESULT 1  
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LOCUS AX147746  
SEQUENCE 523 bp  
DEFINITION AX147746  
ACCESSION AX147746  
VERSION AX147746.1  
KEYWORDS GI:14346791  
SOURCE  
ORGANISM  
rabbit.  
Oryctolagus cuniculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 523)  
Goldspink, G.R. and Johnson, I.R.  
Use of the insulin-like-growth factor I isoform mgf for the  
treatment of neurological disorders

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0136483-A 5 25-MAY-2001;  
University College London (GB)  
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ORIGIN  
Query Match 100.0%; Score 523; DB 6; Length 523;  
Best Local Similarity 100.0%; Pred. No. 2.2e-150;  
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AX300783 523 bp DNA linear PAT 30-NOV-2001  
LOCUS AX300783  
DEFINITION Sequence 5 from Patent WO0185781.  
ACCESSION AX300783  
VERSION AX300783.1 GI:17382064  
KEYWORDS  
SOURCE rabbit.  
ORGANISM Oryctolagus cuniculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
REFERENCE  
1 Goldspink, G.D. and Terenghi, G.B.  
AUTHORS Repair of nerve damage  
TITLE Patent: WO 0185781-A 5 15-NOV-2001;  
JOURNAL

University College London (GB) ; East Grinstead Medical Research  
Trust (GB)  
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BASE COUNT 154 a 129 c 142 g 98 t  
ORIGIN  
Query Match 100.0%; Score 523; DB 6; Length 523;  
Best Local Similarity 100.0%; Pred. No. 2.2e-150;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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AX147742 517 bp DNA linear PAT 08-JUN-2001  
LOCUS AX147742  
DEFINITION Sequence 1 from Patent WO0136483.  
ACCESSION AX147742  
VERSION AX147742.1 GI:14346787  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 (bases 1 to 517)  
AUTHORS Goldspink, G.R. and Johnson, I.R.  
TITLE Use of the insulin-like-growth factor 1 isoform mlf for the  
treatment of neurological disorders

JOURNAL	Patent: WO 0136483-A 1 25-MAY-2001;			
	University College London (GB)			
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Db	481	CAAGATGGCATTTCCCCCAATGAATATCAACAAGTAACAT	521	
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LOCUS	AX300779	517 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO0185781.			
ACCESSION	AX300779			
VERSION	AX300779.1	GI:17382060		
KEYWORDS	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 Goldspink,G.D. and Terenghi,G.B.			
	Repair of nerve damage			
JOURNAL	Patent: WO 0185781-A 1 15-NOV-2001;			

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ORIGIN  
BASE COUNT  
150 a 130 c 139 g 98 t  
Query Match 89.4%; Score 467.4; DB 6; Length 517;  
Best Local Similarity 96.2%; Pred. No. 3.4e-133;  
Matches 501: Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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RESULT 5  
LOCUS AX147754 471 bp DNA linear PAT 08-JUN-2001  
DEFINITION Sequence 13 from Patent WO0136483.  
ACCESSION AX147754  
VERSION AX147754.1 GI:14348552  
KEYWORDS  
SOURCE rabbit.  
ORGANISM Oryctolagus cuniculus  
Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
REFERENCE 1 (bases 1 to 471)  
AUTHORS Goldspink,G.R. and Johnson,I.R.  
TITLE Use of the insulin-like-growth factor I isoform mgf for the  
treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 13 25-MAY-2001;  
 University College London (GB)  
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 BASE COUNT 132 a 118 c 131 g 90 t  
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 Best Local Similarity 90.1%; Pred. No. 3.8e-115;  
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RESULT 6  
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 LOCUS AX300791  
 DEFINITION Sequence 13 from Patent WO0185781.  
 ACCESSION AX300791  
 VERSION AX300791.1 GI:17382072  
 KEYWORDS  
 SOURCE rabbit.  
 ORGANISM Oryctolagus cuniculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus;  
 REFERENCE 1  
 AUTHORS Goldslink, G.D. and Terenghi, G.B.  
 TITLE Repair of nerve damage  
 JOURNAL Patent: WO 0185781-A 13 15-NOV-2001;

University College London (GB) ; East Grinstead Medical Research  
 Trust (GB)  
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 BASE COUNT 132 a 118 c 131 g 90 t  
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 Query Match 78.2%; Score 409; DB 6; Length 471;  
 Best Local Similarity 90.1%; Pred. No. 3.8e-115;  
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 121 ACAGGCACTGCTGATGATGCTGCTTCGGAGCTGTGATGTGAGAGGCTGGAGATGTAC 180  
 Db 121 ACAGGCACTGCTGATGATGCTGCTTCGGAGCTGTGATGTGAGAGGCTGGAGATGTAC 180  
 121 ACAGGCACTGCTGATGATGCTGCTTCGGAGCTGTGATGTGAGAGGCTGGAGATGTAC 180  
 QY 181 TGTGCACCCCTCAAGCCGCGCAAGGCGACGCCGCTCCGTCGCCAGCGCCACACGAC 240  
 181 TGTGCACCCCTCAAGCCGCGCAAGGCGACGCCGCTCCGTCGCCAGCGCCACACGAC 240  
 Db 181 TGTGCACCCCTCAAGCCGCGCAAGGCGACGCCGCTCCGTCGCCAGCGCCACACGAC 240  
 181 TGTGCACCCCTCAAGCCGCGCAAGGCGACGCCGCTCCGTCGCCAGCGCCACACGAC 240  
 QY 241 ATGCCCAAGACTCAGAGTATCAGCCCTCCTACCAACAAGAAATGAAGTCTCAGAGG 300  
 241 ATGCCCAAGACTCAGAGTATCAGCCCTCCTACCAACAAGAAATGAAGTCTCAGAGG 300  
 Db 241 ATGCCCAAGACTCAGAGTATCAGCCCTCCTACCAACAAGAAATGAAGTCTCAGAGG 300  
 241 ATGCCCAAGACTCAGAGTATCAGCCCTCCTACCAACAAGAAATGAAGTCTCAGAGG 300  
 QY 301 AGAAGGAAGAGATACATTGGAAGACACACAGTAGAGGAGTGCAGGAACAGAACTA 360  
 301 AGAAGGAAGAGATACATTGGAAGACACACAGTAGAGGAGTGCAGGAACAGAACTA 360  
 Db 256 -----AAGGAAGTACATTGGAAGACACACAGTAGAGGAGTGCAGGAACAGAACTA 308  
 256 -----AAGGAAGTACATTGGAAGACACACAGTAGAGGAGTGCAGGAACAGAACTA 308  
 QY 361 CAGGATGTAGGAAGACCCCTCTGAGAGGTGAAGAAGACAGGCCACCGCAGACCTTTG 420  
 361 CAGGATGTAGGAAGACCCCTCTGAGAGGTGAAGAAGACAGGCCACCGCAGACCTTTG 420  
 Db 309 CAGGATGTAGGAAGACCCCTCTGAGAGGTGAAGAAGACAGGCCACCGCAGACCTTTG 368  
 309 CAGGATGTAGGAAGACCCCTCTGAGAGGTGAAGAAGACAGGCCACCGCAGACCTTTG 368  
 QY 421 CTCTGCACAGTTACCTGTAAACATTTGAATACCGGCCAAAATTAAGTTGATCATTG 480  
 421 CTCTGCACAGTTACCTGTAAACATTTGAATACCGGCCAAAATTAAGTTGATCATTG 480  
 Db 369 CTCTGCACAGTTACCTGTAAACATTTGAATACCGGCCAAAATTAAGTTGATCATTG 428  
 369 CTCTGCACAGTTACCTGTAAACATTTGAATACCGGCCAAAATTAAGTTGATCATTG 428  
 QY 481 CAAAGATGGCATTTCGCCCAATGAATACACAAGTAACATTG 523  
 481 CAAAGATGGCATTTCGCCCAATGAATACACAAGTAACATTG 523  
 Db 429 CAAAGATGGCATTTCGCCCAATGAATACACAAGTAACATTG 471  
 429 CAAAGATGGCATTTCGCCCAATGAATACACAAGTAACATTG 471

RESULT 7  
 BC012409 1536 bp mRNA linear ROD 07-AUG-2002  
 LOCUS BC012409  
 DEFINITION Mus musculus, Similar to insulin-like growth factor 1, clone  
 MGC:18617 IMAGE:4194295, mRNA, complete cds.  
 ACCESSION BC012409  
 VERSION BC012409.1 GI:15214568  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission



Db 337 ACGGCGATGTTGATGATGTTGCTTCCGAGCTGTGATCTGAGGAGCTGAGATGTAC 396  
 QY 181 TGTGACCCCTTCACCGCGGCAAGGACCGGCTCGCTGCGGCCGCGCACACGAC 240  
 Db 397 TGTGCTCGCGTGAAGCCTACAACTGACGTGTTCCCTCCGCGGCCGCGCACACGAC 456  
 QY 241 ATGCCCAAGACTGAGAGTATCAGCTTCATCTACCAACAAGAAATGAGTCTCAGAG 300  
 Db 457 ATGCCCAAGACTGAGAGTATCAGCTTCATCTACCAACAAGAAATGAGTCTCAGAG 516  
 QY 301 AGAAGGAAGAACTTACATTTGAAGAACACAGTAGAGGGAGTGCAGAAACAAGACTA 360  
 Db 517 AGAAGGAAGAACTTACATTTGAAGAACACAGTAGAGGGAGTGCAGAAACAAGACTA 576  
 QY 361 CAGAGTGTAGAGAACCCCTCTGAGAGTGAAGAGAGAGCCACCGACGACCTTTG 420  
 Db 577 CAGAGTGTAGAGAGAGCCCTCCGAGAGAACAGAAATGCTCACCGCAGAGATCTTTG 636  
 QY 421 CTGTGCAAGCTTACCTGTAACCATTTGAAATACGAGCA-----AAAATAGTTGATC 474  
 Db 637 CTGTGCAAGCACTGCAAAACATCGAACACCTGCGCAATATCATATGATGATCAATA 696  
 QY 475 ACATTTCAAGAT-GGCATTTCCCGCAATGAATACACAGTAACATTC 523  
 Db 697 CCATTTCAAGATGGCATTTCCCTCAATGAATACACAGTAACATTC 746

RESULT 9  
 RNTGFI1  
 LOCUS RNTGFI1 958 bp mRNA linear ROD 12-SEP-1993  
 DEFINITION Rat mRNA (clone IGF1AB1) for insulin-like growth factor I.  
 ACCESSION X06107 M32260 Y00429  
 VERSION X06107.1 GI:56424  
 KEYWORDS insulin-like growth factor I.  
 SOURCE Rattus norvegicus.  
 ORGANISM Rattus norvegicus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 958)  
 AUTHORS Rotwein P.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-OCT-1987) Rotwein P., Washington University, School of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO 63110, USA  
 REFERENCE 2 (bases 1 to 958)  
 AUTHORS Shimatsu A. and Rotwein P.  
 TITLE Sequence of two rat insulin-like growth factor I mRNAs differing within the 5' untranslated region  
 JOURNAL Nucleic Acids Res. 15 (17), 7196 (1987)  
 MEDLINE 8801572  
 PUBMED 3658684  
 COMMENT Another IGF-I mRNA of rat liver differing in the 5' UT-region is described in <X06108>.

FEATURES  
 source  
 1..958  
 /organism="Rattus norvegicus"  
 /strain="Strague-Dawley"  
 /db\_xref="taxon:10116"  
 /tissue\_type="liver"  
 1..258  
 /note="5' UT-region"  
 259..738  
 /note="IGF-I (AA 1-159)"  
 /codon\_start=1  
 /protein\_id="CAA29480.1"  
 /db\_xref="GI:56425"  
 /db\_xref="SMISS-PROT:P08024"  
 /translation="MGKISSLPOLFKICLDFKIKIHSSSHLYALCLITFTS  
 SATAGETLCAELVDALQGVCPGPFVFNKPTGYSIRAPOTGIIVDECCPRSDL  
 RLLEMYCAPLKPITSARSIRNRHNDMKTKQSPLSLHKRKLORRKRSTLEHNR"  
 739..958  
 /note="3' UT-region"  
 misc-feature  
 misc-feature  
 736..958  
 /note="3' UT-region"

BASE COUNT 260 a 246 c 209 g 243 t  
 ORIGIN  
 Query Match 69.1%; Score 361.6; DB 10; Length 958;  
 Best Local Similarity 82.8%; Pred. No. 1.9e-100;  
 Matches 439; Conservative 0; Mismatches 84; Indels 7; Gaps 2;

QY 1 GGCACGAGACGCTCTGCGGTCTGTGAGTGTGATGCTCTTCACTGCTGTGGAGAC 60  
 Db 403 GGCACGAGACGCTCTGCGGTCTGTGAGTGTGATGCTCTTCACTGCTGTGGAGAC 462  
 QY 61 AGGGGCTTTTATTTCACAGCCACAGAGTACGGCTCAGAGTCGAGGCGACCTTACG 120  
 Db 463 AGGGGCTTTTATTTCACAGCCACAGAGTATGCTCAGAGTTCGAGGCGACACAG 522  
 QY 121 ACAGGCTGTGAGTGTGCTGCTTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 180  
 Db 523 ACAGGCTGTGAGTGTGCTGCTTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 582  
 QY 181 TGTGCAAGCTTACAGCGGCAAGAGCAGCGCTCGTCCGTCGCGCAGGCGCAC 240  
 Db 583 TGTGCTCCCTGAGGCTTCAAAAGTACGCTCTTCATCAGGCGCCAGCGCACACTAC 642  
 QY 241 ATGCCCAAGACTGAGAGTATCAGCTTCATCTACCAACAAGAAATGATGTGAGAG 300  
 Db 643 ATGCCCAAGACTGAGAGTATCAGCTTCATCTACCAACAAGAAATGATGTGAGAG 702  
 QY 301 AGAAGGAAGGAAGTATGATGAGAACACAGTAGAGGAGTGCAGAGAAACAAGACTA 360  
 Db 703 AGAAGGAAGGAAGTATGATGAGAACACAGTAGAGGAGTGCAGAGAAACAAGACTA 762  
 QY 361 CAGAGTGTAGAGAACCCCTTCTGAGAGTGAAGAGAGAGCCACCGCAGGACCTTTG 420  
 Db 763 CAGAGTGTAGAGAGAGCCCTCCGAGAGAACAGAAATGCCACGTCACCGCAAGATCTTTG 822  
 QY 421 CTGTGCAAGCTTACCTGTAACCATTTGAAATACGAGCA-----AAAATAGTTGATC 474  
 Db 823 CTGTGCAAGCACTGCAAAACATCGAACACCTGCGCAATATCATATGATGATCAATA 882

RESULT 10  
 RATIGFIA  
 LOCUS RATIGFIA 710 bp mRNA linear ROD 27-APR-1993  
 DEFINITION Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.  
 ACCESSION M15480  
 VERSION M15480.1 GI:204749  
 KEYWORDS growth factor; insulin-like growth factor.  
 SOURCE Rat (Sprague-Dawley) adult liver cDNA to mRNA, clone PRIGF-1-42.  
 ORGANISM Rattus norvegicus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 710)  
 AUTHORS Roberts C.T. Jr., Lasky S.R., Lowe W.L. Jr., Seaman W.T. and Leroult D.  
 TITLE Molecular cloning of rat insulin-like growth factor I complementary deoxyribonucleic acids: differential messenger ribonucleic acid processing and regulation by growth hormone in extrahypophyseal tissues  
 JOURNAL Mol. Endocrinol. 1 (3), 243-248 (1987)  
 MEDLINE 88288198  
 PUBMED 3453891  
 COMMENT Draft entry and computer-readable copy of sequence in [Mol. Endocrinol. (1987) in press] kindly provided by S.R.Lasky, 16-MAR-1987.  
 FEATURES  
 source  
 1..710  
 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 CDS  
 106..507

RESULT 11	AX147744	LOCUS	AX147744	539 bp	DNA	linear	PAT 08-JUN-2001
DEFINITION	Sequence 3 from Patent WO0136483.						
ACCESSION	AX147744						
VERSION	AX147744.1	GI:14346789					
KEYWORDS							
SOURCE	Norway rat.						
ORGANISM	Rattus norvegicus						
	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;						

RESULT 12				
AX300781	AX300781	539 bp	DNA	linear
LOCUS	Sequence 3 from Patent WO0185781.			
DEFINITION	AX300781			
ACCESSION	AX300781.1	GI:17382062		
VERSION				
KEYWORDS				
SOURCE	Rattus sp.			
ORGANISM	Rattus sp.			

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.  
 Goldspink, G.D. and Terenghi, G.B.  
 Repair of nerve damage  
 Patent: WO 0185781-A 3 15-NOV-2001;  
 University College London (GB) ; East Grinstead Medical Research Trust (GB)  
 Location/Qualifiers  
 1..539  
 /organism="Rattus sp."  
 /db\_xref="taxon:10118"  
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 /note="unnamed protein product"  
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 /protein\_id="CAD3041.1"  
 /db\_xref="GI:17382063"  
 /translation="GPEITGLAEVDALEQVCGRGRFYENKPTVYSSIRAPQGTIV DECCFRSCDRLRLEMYCVRCKPTKSARSIRARHTDMPKQKSQPLSTHKRRLQRRR KSTLEERK"  
 BASE COUNT 16: a 136 c 139 g 103 t  
 ORIGIN  
 Query Match 68.2%; Score 356.8; DB 6; Length 539;  
 Best Local Similarity 82.3%; Pred. No. 5.4e-99;  
 Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;  
 1 GGACCGGAGACGCTGCGGCTGCTGAGTGTGATGCTCTTCAGTTCGTGTGGAGAC 60  
 1 GGACCGAGAGACCTTTGGGGCTGAGCTGATGACCTCTTCAGTTCGTGTGGAGAC 60  
 61 AGGGCTTTTATTTCAACAGACCCACAGATACGCTCCAGCAGCTCGAGGACCTCAG 120  
 61 AGGGCTTTTACTTCAACAGACCCACAGATACGCTCCAGCAGCTCGAGGACCTCAG 120  
 61 AGGGCTTTTACTTCAACAGACCCACAGATACGCTCCAGCAGCTCGAGGACCTCAG 120  
 121 ACAGGACATCGTGATGATGCTGCTCCGAGCTGTATGATGAGAGAGCTGGAGATGAT 180  
 121 ACAGGACATGATGATGATGCTGCTCCGAGCTGTATGATGAGAGAGCTGGAGATGAT 180  
 121 ACAGGACATGATGATGATGCTGCTCCGAGCTGTATGATGAGAGAGCTGGAGATGAT 180  
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 181 TGTGACCCCTCAAGCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG 240  
 181 TGTGACCCCTCAAGCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG 240  
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 241 ATGCCCAAGACTCAGAAATATCAGCTTCATCTACCAACAAGAAATGAAGTCTCAAG 300  
 301 AGAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
 301 AGAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
 361 CAGAGTGTAGAGAGACCTTCTGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 420  
 361 CAGAGTGTAG 420  
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 421 CTCTGACAGTGTACCTGTAACATTTGGAATACCGGCA-----AAAAATGAAGTAT 474  
 421 CTCTGACAGTGTACCTGTAACATTTGGAATACCGGCA-----AAAAATGAAGTAT 474  
 421 CTCTGACAGTGTACCTGTAACATTTGGAATACCGGCA-----AAAAATGAAGTAT 474  
 475 ACATTTCAAGAT-GGCATTTCCCAATGAATACAGCAAGTAAATC 523  
 475 ACATTTCAAGAT-GGCATTTCCCAATGAATACAGCAAGTAAATC 523  
 481 TCATTTCAAGATGGGCAATTTCCCAATGAATACAGCAAGTAAATC 530  
 481 TCATTTCAAGATGGGCAATTTCCCAATGAATACAGCAAGTAAATC 530  
 RESULT 13  
 MMIF1BR 651 bp mRNA linear ROD 21-MAR-1995  
 LOCUS MMIF1BR 651 bp mRNA linear ROD 21-MAR-1995  
 DEFINITION Mouse mRNA for preproinsulin-like growth factor IB.  
 X04482  
 X04482.1 GI:51806  
 VERSION  
 KEYWORDS growth factor; insulin-like growth factor IB; preproinsulin-like growth factor IB; signal peptide.

SOURCE Mus musculus.  
 ORGANISM Mus musculus.  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus. 1 (bases 1 to 651)  
 Bell, G.I., Stempien, M.M., Fong, N.M. and Rall, L.B.  
 Sequences of liver cDNAs encoding two different mouse insulin-like growth factor I precursors  
 Nucleic Acids Res. 14 (20), 7873-7882 (1986)  
 JOURNAL 87040760  
 MEDLINE 3774549  
 PUBMED  
 COMMENT  
 The sequence is identical to the preproIGF-1A sequence (X04480) except for the presence of a 52 bp insertion following codon 86 (position 397 to 448), caused by alternative RNA splicing. The B domain of IGF comprises residues 1-29 (position 138-225). The C domain residues 30-41 (position 226-261), the A domain residues 42-62 (position 262-324) and the D domain residues 63-70 (position 325-348).  
 Location/Qualifiers  
 1..651  
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 /strain="Balb/c"  
 /db\_xref="taxon:10090"  
 /clone="migf1-4"  
 /tissue="liver"  
 43..45  
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 73..474  
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 /protein\_id="CAA28170.1"  
 /db\_xref="GI:51807"  
 /db\_xref="MGI:96432"  
 /db\_xref="SWISS-PROT:P05018"  
 /translation="MSSSLFLALCLLFTSTAGPETLGAELVALQVCGPRG FYENKPTVYSSIRAPQGTIVDECCFRSCDRLRLEMYCVRCKPTKSARSIRARHTD MPKQKSQPLSTHKRRLQRRRSGTFEERK"  
 73..138  
 139..348  
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 mat-peptide  
 misc-feature  
 /product="mature IGF-1B (aa 1-70)"  
 349..471  
 /note="COOH-terminal peptide (E domain) (aa 71 to 111)"  
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 /note="polyA site"  
 BASE COUNT 193 a 185 c 149 g 124 t  
 ORIGIN  
 Query Match 66.8%; Score 349.4; DB 10; Length 651;  
 Best Local Similarity 82.8%; Pred. No. 1.1e-96;  
 Matches 425; Conservative 0; Mismatches 81; Indels 7; Gaps 2;  
 1 GGACCGGAGACGCTGCGGCTGCTGAGTGTGATGCTCTTCAGTTCGTGTGGAGAC 60  
 139 GGACCGAGAGACCTTTGGGGCTGAGCTGATGAGCTCTTCAGTTCGTGTGGAGAC 198  
 61 AGGGCTTTTATTTCAACAGACCCACAGATACGCTCCAGAGTGGAGGACCTCAG 120  
 199 AGGGCTTTTACTTCAACAGACCCACAGATACGCTCCAGAGTGGAGGACCTCAG 258  
 61 AGGGCTTTTATTTCAACAGACCCACAGATACGCTCCAGAGTGGAGGACCTCAG 120  
 199 AGGGCTTTTACTTCAACAGACCCACAGATACGCTCCAGAGTGGAGGACCTCAG 258  
 121 ACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
 259 ACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 318  
 181 TGTGACCCCTCAAGCCGCAAGGACAGCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 240  
 319 TGTGACCCCTCAAGCCGCAAGGACAGCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 378  
 241 ATGCCCAAGACTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 379 ATGCCCAAGACTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 438  
 301 AGAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360



Db 439 AGAAGGAAGAGTACATTTTGAAGAACACAGTAGAGAGTGCAGGAAGACAGCTA 498  
QY 361 CAGATGTAGAGAGACCTTTCTAGAGAGTGAAGAGACAGGCCACCGAGAGACCTTTG 420  
Db 499 CAGAAAGTAGAGAGACCTTCCACAGAGAGAAAGAACACATCACCGAGATCCTTTG 558  
QY 421 CTCTGCACAGATTCCTGTAAACATTTGATACCGGCCA-----AAAATAAGTTGATC 474  
Db 559 CTGCTTGAGAGACCTTGCAGAAACATTCAGAACACCTTACCAGTAATTAATAGTCCATA 618  
QY 475 ACATTTCAAGAT-GGCATTTCCCAATGAAA 506  
Db 619 ACATTTCAAGATGGCATTTCCCAATGAAA 651

RESULT 14  
AF022961 432 bp mRNA linear MAY 14-OCT-1997  
LOCUS AF022961  
DEFINITION Oryctolagus cuniculus insulin-like growth factor IB (IGF-IB) mRNA,  
complete cds.  
ACCESSION AF022961  
VERSION AF022961.1 GI:2522201  
KEYWORDS Oryctolagus cuniculus.  
SOURCE Oryctolagus cuniculus.  
ORGANISM Oryctolagus cuniculus.  
REFERENCE 1 (bases 1 to 432)  
AUTHORS Flekna,G., Brem,G. and Mueller,M.  
TITLE Direct Submission  
JOURNAL Submitted (05-SEP-1997) Institute of Animal Breeding and Genetics,  
Veterinary University of Vienna, Veterinaerplatz 1, Vienna A-1210,  
Austria

FEATURES  
source Location/Qualifiers  
1..432  
/organism="Oryctolagus cuniculus"  
/strain="Zika hybrid strain"  
/db\_xref="taxon:9986"  
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/tissue\_type="liver"  
1..432  
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1..432  
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/codon\_start=1  
/product="insulin-like growth factor IB"  
/protein\_id="AAB80950.1"  
/db\_xref="GI:2522202"  
/translation="MTPTVKKRIILSSHLFYALCLLFTSSATGAPTLLGAEIYD  
ALQFVGDSGFYFNKRTGYGSSRRAPQGTGYDECCFRGCDLRLRLMTCAPIKPAKAA  
RSVRAQRHIDMFTQYQPPSTVKMKSSRRRKGSTFEHK"

BASE COUNT 105 a 126 c 115 g 86 t

ORIGIN  
Query Match 64.2%; Score 336; DB 4; Length 432;  
Best Local Similarity 100.0%; Pred. No. 1.4e-92;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACCGAGACGCTGCGGCTGCTGAGCTGCTGATGCTTTCATGCTGCTGAGAG 60  
Db 97 GGACCGAGAGCGCTGCGGCTGCTGAGCTGCTGATGCTTTCATGCTGCTGAGAG 156  
QY 61 AGGGGCTTTTATTTCAACAAGCCACAGATAGGGCTCAGAGCTGGAGGGAGACTGAG 120  
Db 157 AGGGGCTTTTATTTCAACAAGCCACAGATAGGGCTCAGAGCTGGAGGGAGACTGAG 216  
QY 121 ACAAGCATGTGATGATGCTGCTCCGAGCTGTGATCTGAGAGGCTGGAGATGTAC 180  
Db 217 ACAAGCATGTGATGATGCTGCTCCGAGCTGTGATCTGAGAGGCTGGAGATGTAC 276  
QY 181 TGTGACCCCTCAAGCGCGAAGGACAGCCCGCTCGCTCCGACAGGCGCCACAGCGAG 240  
Db 277 TGTGACCCCTCAAGCGCGAAGGACAGCCCGCTCGCTCCGACAGGCGCCACAGCGAG 336

QY 241 ATGCCCAAGACTCAAAAGTATCAGCTCCATCTACCAACAAGAAATGAGTCTCAGAG 300  
Db 337 ATGCCCAAGACTCAAAAGTATCAGCTCCATCTACCAACAAGAAATGAGTCTCAGAG 396  
QY 301 AGAAGGAAGGAAGTACATTTGAAGACACAAGTAG 336  
Db 397 AGAAGGAAGGAAGTACATTTGAAGACACAAGTAG 432

RESULT 15  
AX375028 7260 bp DNA linear PAT 01-MAR-2002  
LOCUS AX375028  
DEFINITION Sequence 31 from Patent WO0210436.  
ACCESSION AX375028  
VERSION AX375028.1 GI:19169860  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Baak,J. and Mutter,G.L.  
TITLE Prognostic classification of breast cancer  
JOURNAL Patent: WO 0210436-A 31 07-FEB-2002;  
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US)

FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 2330 a 1415 c 1240 g 2275 t

ORIGIN  
Query Match 63.9%; Score 334.4; DB 6; Length 7260;  
Best Local Similarity 84.6%; Pred. No. 6.7e-92;  
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

QY 1 GGACCGAGACGCTGCGGCTGCTGAGCTGCTGATGCTTTCATGCTGCTGAGAG 60  
Db 311 GGACCGAGAGCGCTGCGGCTGCTGAGCTGCTGATGCTTTCATGCTGCTGAGAG 370  
QY 61 AGGGGCTTTTATTTCAACAAGCCACAGATAGGGCTCAGAGCTGGAGGGAGGAGCCCTCAG 120  
Db 371 AGGGGCTTTTATTTCAACAAGCCACAGATAGGGCTCAGAGCTGGAGGGAGGAGCCCTCAG 430  
QY 121 ACAGGATCGTGTGATGATGCTGCTTCCGAGCTGTGATCTGAGAGGCTGGAGATGTAC 180  
Db 431 ACAGGATCGTGTGATGATGCTGCTTCCGAGCTGTGATCTGAGAGGCTGGAGATGTAT 490  
QY 181 TGTGACCCCTTAAGCCGGAAGGACAGCCCGCTCCGTCGTCGCCAGCCACAGCCAG 240  
Db 491 TGTGACCCCTTAAGCCGGAAGGACAGCCCGCTCCGTCGTCGCCAGCCACAGCCAG 550  
QY 241 ATGCCCAAGACTCAAAAGTATCAGCTCCATCTACCAACAAGAAATGAGTCTCAGAG 300  
Db 551 ATGCCCAAGACTCAAAAGTATCAGCTCCATCTACCAACAAGAAATGAGTCTCAGAG 565  
QY 301 AGAAGGAAGGAAGTACATTTGAAGACACAAGTAGAGAGGAGTGCAGAGAAACAAGACTA 360  
Db 566 -----AAGGAGTACATTTGAAGACACAAGTAGAGGAGTGCAGAGAAACAAGACTA 618  
QY 361 CAGATGTAGAGAGACCTTCTGAGAGTGAAGAAGACAGAGCCACCGCAGAGACCTTG 420  
Db 619 CAGATGTAGAGAGACCTTCTGAGAGTGAAGAAGTGAAGATGACATGCCACCGCAGATCTTG 678  
QY 421 CTCTGCAC-AGTTACCTG-TAAACATGGAATACCGGCGCAAAAATAAGTTGATCAT 478  
Db 679 CTCTGCACAGATTACCTGTTAACTTTGGAACACCTTACCAAAAATAAGTTGATACAT 738  
QY 479 TTCAAGAT-GGCATTTCCCAATGAATACAGAGTAACATTC 523  
Db 739 TTAAAGATGGCGTTTCCCAATGAATACAGAGTAACATTC 784

Mon Jun 16 09:51:44 2003

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Page 10

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Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

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Listing first 45 summaries

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6: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
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14: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
15: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
16: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
17: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
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19: /SID82/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
20: /SID82/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
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22: /SID82/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
23: /SID82/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
24: /SID82/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	100.0	523	22	AA06400
2	523	100.0	523	22	AA06400
3	523	100.0	523	18	AA06400
4	467.4	89.4	517	22	AA06398
5	467.4	89.4	517	22	AA06398
6	409	78.2	471	22	AA06405
7	409	78.2	471	22	AA06405
8	356.8	68.2	539	22	AA06399
9	356.8	68.2	539	24	AA06399

10	334.4	63.9	818	8	AA070435	Sequence encoding
11	334.4	63.9	7260	24	ABK84583	Human cDNA differe
12	334.4	63.9	7260	24	ABN97244	Gene #3742 used to
13	334.4	63.9	7260	24	ABK64812	Human benign prost
14	334.4	63.9	7260	24	ABK55504	Human endometrial
15	334.4	63.9	7260	24	ABK55511	Gene IGF1 differer
16	332.8	63.6	777	18	AA048894	Human insulin-like
17	331.2	63.3	622	7	AA060490	Human prepro-somat
18	281.8	53.9	978	14	AA047804	Sequence encoding
19	275.2	52.6	1136	8	AA070435	Sequence encoding
20	274.6	52.5	3599	19	AAV50428	Plasmid pIG0552 to
21	274.6	52.5	3599	19	AAV40796	Actual sequence of
22	274.6	52.5	3600	19	AAV50427	Plasmid pIG0552 up
23	274.6	52.5	3600	19	AAV40795	Expected sequence
24	274.6	52.5	5707	20	AAV88054	Plasmid pIG0335 DN
25	274.6	52.5	6345	20	AAV88054	Plasmid pIG0100A D
26	273.6	52.3	612	22	AA014695	Human cDNA encodin
27	268.8	50.1	1052	20	AA027498	Rat liver form of
28	262	50.1	487	22	AA06404	Rat insulin-like IGF
29	262	50.1	487	22	AA06404	Rat insulin-like IGF
30	237.6	45.4	317	24	AA06403	Human liver-type I
31	237.6	45.4	318	22	AA06403	Human liver-type I
32	237.6	45.4	462	19	AAV50426	Human IGF-1 encodi
33	237.6	45.4	462	19	AAV40794	Human IGF-1 coding
34	237.6	45.4	462	24	ABK91699	Human polynucleoti
35	193	36.9	210	24	ABK03146	Native mature IGF-
36	191.4	36.6	237	12	AA03568	Beta-gal/IGF-1 fus
37	191.4	36.6	238	12	AA03569	Recombinant botuli
38	181.4	36.6	2862	19	AAV26283	Recombinant botuli
39	187	35.8	4532	24	AA032015	Bovine alpha lacta
40	186.6	35.7	210	24	AA032016	Human insulin-like
41	185.2	35.4	240	13	AA023303	Synthetic human IG
42	185.2	35.4	390	19	AA063526	Killer toxin leade
43	183.4	35.1	462	18	AAV50425	Human IGF-1 encodi
44	183.4	35.1	462	19	AAV40793	Optimised IGF-1 co
45	180.2	34.5	207	22	AA022139	Truncated human in

#### ALIGNMENTS

RESULT 1	AA06400	standard; cDNA: 523 BP.
ID	AA06400	
AC	AA06400	
XX	10-AUG-2001	(first entry)
DT		
XX		
DE		Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.
XX		
KW		Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW		mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW		amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW		poliomyelitis; post-polio syndrome; toxin; motoneuron disorder;
KW		nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW		new-linked muscular dystrophy; peripheral neuropathy;
KW		Alzheimer's disease; Parkinson's disease; ss.
XX		
OS		Oryctolagus cuniculus.
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..336
FT		/*tag= a
FT		/product= "Mechano-growth factor (MGF) "
FT		/note= "This region comprises exons 3-6. The CDS does
FT		not include start codon"
XX		/partial
XX		
XX		WO200136483-A1.
XX		25-MAY-2001.

PF 15-NOV-2000; 2000WO-GB04354.  
 XX  
 PR 15-NOV-1999; 99GB-0026968.  
 XX  
 XX (UNLO ) UNIV COLLEGE LONDON.  
 XX  
 PI Goldslink G, Johnson I;  
 XX  
 DR WPI: 2001-355620/37.  
 DR P-PSDB: AAE02449.  
 XX  
 PT Use of mechano-growth factor, an isoform of insulin-like Growth  
 PT Factor-I, capable of reducing motoneuron loss, in the manufacture of a  
 PT medicament for the treatment of neurological disorder -  
 XX  
 PS Claim 4; Page 53-54; 66pp; English.  
 CC The present invention relates to use of mechano-growth factor (MGF),  
 CC an insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a  
 CC medicament for the treatment of neurological disorder. The MGF is capable  
 CC of reducing motoneuron loss by 20% or greater in response to nerve  
 CC avulsion, and effects motoneuron rescue, preferably adult motoneuron  
 CC rescue. The MGF polynucleotide and polypeptide are useful in the  
 CC manufacture of a medicament for the treatment of a neurological disorder,  
 CC including a disorder of motoneurons and/or neurodegenerative disorder,  
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive  
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,  
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a  
 CC toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an  
 CC injury that affects motoneurons, motoneuron loss associated with aging,  
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,  
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.  
 CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle  
 CC isoform having extracellular (Ec) domain, hence also referred as  
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by  
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame  
 CC of MGF.  
 XX  
 SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;  
 Query Match 100.0%; Score 523; DB 22; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-144;  
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 421 CTTGCGACAGTTACTGTAACATTGGAAATACCGGCCCAAAATAAGTTGATCATTT 480  
 QY 481 CAAGATGGCAATTTCCCAATGAATAACAGTAACATTC 523  
 DB 481 CAAGATGGCAATTTCCCAATGAATAACAGTAACATTC 523  
 RESULT 2  
 AAS16879  
 ID AAS16879 standard; cDNA; 523 BP.  
 XX  
 AC AAS16879;  
 XX  
 DT 25-FEB-2002 (first entry)  
 DE Rabbit mechano-growth factor (MGF) cDNA.  
 XX  
 XX Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;  
 KM neuroprotective; nerve damage; peripheral nervous system; nerve severing;  
 KM muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;  
 KM nerve avulsion.  
 XX  
 OS Oryctolagus cuniculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..336  
 FT /tag= a  
 FT /product= "Rabbit MGF"  
 FT /partial  
 FT /note= "No start codon"  
 FT exon 1..76  
 FT /tag= b  
 FT /number= 3  
 FT exon 77..259  
 FT /tag= c  
 FT /number= 4  
 FT exon 260..309  
 FT /tag= d  
 FT /number= 5  
 FT exon 311..333  
 FT /tag= e  
 FT /number= 6  
 XX  
 PN WO200185781-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PE 10-MAY-2001; 2001WO-GB02054.  
 PR 10-MAY-2000; 2000GB-0011278.  
 XX  
 PA (UNLO ) UNIV COLLEGE LONDON.  
 PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.  
 XX  
 PI Goldslink G, Terenigh G;  
 XX  
 DR WPI: 2002-055585/07.  
 DR P-PSDB: AAU10561.  
 XX  
 PT Use of insulin-like growth factor I (IGF-I) isoform known as  
 PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has  
 PT ability to reduce motoneuron loss in response to nerve avulsion, to  
 PT treat nerve damage  
 XX  
 PS Disclosure; Fig 7; 65pp; English.  
 XX  
 CC The invention relates to the use of an insulin-like growth factor I  
 CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture  
 CC of a medicament for treating nerve damage in the peripheral nervous  
 CC system, or for treating nerve damage by localising MGF at the site of  
 CC damage. The nerve damage may include severing of a nerve. The treatment  
 CC may be combined with another treatment (such as a polypeptide growth



Db 511 CAAAGATGGCATTTCGCCCAATGAATAACACAGTAACATTTC 553

RESULT 4  
ADD06398  
ID ADD06398 standard; cDNA: 517 BP.

XX  
AC AAD06398;  
XX  
DT 10-AUG-2001 (first entry)

XX  
DE Human IGF-I isoform mechano-growth factor (MGF) cDNA.

XX  
KW Human: IGF-I isoform; Insulin-like Growth Factor-I; MGF;  
KW mechano-growth factor; neurological disorder; neurodegenerative disorder;  
KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;  
KW polyomyelitis; post-polio syndrome; toxin; motoneuron disorder;  
KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;  
KW sex-linked muscular dystrophy; peripheral neuropathy;  
KW Alzheimer's disease; Parkinson's disease; ss.

XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT CDS 1..333  
FT /tag= a  
FT /product= "Mechano-growth factor (MGF)"  
FT /note= "This region comprises exons 3-6. The CDS does  
FT not include start codon"  
FT /partial

XX  
PN MO200136483-A1.

XX  
PD 25-MAY-2001.

XX  
PF 15-NOV-2000; 2000MO-GB04354.

XX  
PR 15-NOV-1999; 99GB-0026968.

XX  
PA (UNLO ) UNIV COLLEGE LONDON.

XX  
PI Goldspeak G, Johnson I;

XX  
DR WPI: 2001-355620/37.  
DR P-PSDB; AAE02447.

XX  
PT Use of mechano-growth factor, an isoform of insulin-like Growth  
PT Factor-I, capable of reducing motoneuron loss, in the manufacture of a  
PT medicament for the treatment of neurological disorder -

XX  
PS Claim 4; Page 49-50; 66pp; English.

XX  
CC The present invention relates to use of mechano-growth factor (MGF),  
CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a  
CC medicament for the treatment of neurological disorder. The MGF is capable  
CC of reducing motoneuron loss by 20% or greater in response to nerve  
CC avulsion, and effects motoneuron rescue, preferably adult motoneuron  
CC rescue. The MGF polynucleotide and polypeptide are useful in the  
CC manufacture of a medicament for the treatment of a neurological disorder,  
CC including a disorder of motoneurons and/or neurodegenerative disorder,  
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive  
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,  
CC polyomyelitis or post-polio syndrome, a disorder caused by exposure to a  
CC toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an  
CC injury that affects motoneurons, motoneuron loss associated with aging,  
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,  
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.  
CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle  
CC isoform having extracellular (EC) domain, hence also referred as  
CC IGF-I-EC. The MGF protein comprises amino acid sequences encoded by  
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame  
CC of MGF.

SO Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 89.4%; Score 467.4; DB 22; Length 517;  
Best Local Similarity 96.2%; Pred. No. 1,35e-127;  
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

QY 1 GGACGGAGAGAGCTCTGCGTGTGAGCTGTGATGCTGCTTTCAGTTGTTGTGAGAG 60  
DB 1 GGACGGAGAGAGCTCTGCGGCTGTGAGCTGTGATGCTGCTTTCAGTTGTTGTGAGAG 60  
QY 61 AGGAGCTTTTATTTCACCAAGCCACAGATAGAGCTTCCAGAGTGGAGAGCACTCAG 120  
DB 61 AGGAGCTTTTATTTCACCAAGCCACAGATAGAGCTTCCAGAGTGGAGAGCACTCAG 120  
QY 121 ACAGGATCGTGTGATGAGTCTGCTCTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 180  
DB 121 ACAGGATCGTGTGATGAGTCTGCTCTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 180  
QY 181 TGTGACCCCTCAAGCCGCAAGAGGACGCCCTCCGCTCCGTCGCCAGCCACACCGAC 240  
DB 181 TGTGACCCCTCAAGCCGCAAGAGGACGCCCTCCGCTCCGTCGCCAGCCACACCGAC 240  
QY 241 ATGCCCAAGACTGAGATATCAGCTCAGCTCCTATACCAAGAAATGAAGTCTCAGAG 300  
DB 241 ATGCCCAAGACTGAGATATCAGCTCCTATACCAAGAAATGAAGTCTCAGAG 300  
QY 301 AGAAGAAAGAAAGTACATTGGAAGAACACAGTAGAGGAGTGCAAGAAACAAAGACTA 360  
DB 298 AGAAGAAAGAAAGTACATTGGAAGAACACAGTAGAGGAGTGCAAGAAACAAAGACTA 357  
QY 361 CAGATGTAGAAAGACCTCTCTGAGAGTGAAGAGGACGCGCAGGACCCCTTG 420  
DB 358 CAGATGTGA-GAAGACCTCTCTGAGAGTGAAGAGGACGCGCAGGACCCCTTG 416  
QY 421 CTCTGCACAGTTACCTTAACATTTGGAATACCGGCGCAAAAATAATTGATGACATT 480  
DB 417 CTCTGCACAGTTACCTTAACATTTGGAATACCGGCGCAAAAATAATTGATGACATT 476  
QY 481 CAAAGATGGCATTTCGCCCAATGAATAACACAGTAACAT 521  
DB 477 CAAAGATGGCATTTCGCCCAATGAATAACAGTAACAT 517

RESULT 5  
AAS16877  
ID AAS16877 standard; cDNA: 517 BP.

XX  
AC AAS16877;  
XX  
DT 25-FEB-2002 (first entry)

XX  
DE Human mechano-growth factor (MGF) cDNA.

XX  
KW Human: mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;  
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;  
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;  
KW nerve avulsion.

XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT CDS 1..333  
FT /tag= a  
FT /product= "Human MGF"  
FT /note= "No start codon"  
FT /partial  
FT /number= 3  
FT /tag= b  
FT /number= 3  
FT /tag= c  
FT /number= 4  
FT /tag= c  
FT /number= 4  
FT exon  
FT exon  
FT exon

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FT      /tag= d
FT      /number= 5
FT      308..330
FT      /tag= e
FT      /number= 6
XX      WO200185781-A2.
XX      15-NOV-2001.
XX      10-MAY-2001: 2001WO-GB02054.
XX      10-MAY-2000: 2000GB-0011278.
XX      (UNLO ) UNIV COLLEGE LONDON.
XX      (EGR1-) EAST GRINSTEAD MEDICAL RES TRUST.
XX      Goldslink G, Terenghl G;
XX      WPI: 2002-055585/07.
XX      P-PSDB: AAU10559.
XX      Use of insulin-like growth factor I (IGF-I) isoform known as
XX      mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
XX      ability to reduce motoneuron loss in response to nerve avulsion, to
XX      treat nerve damage.
XX      Claim 11, Fig 5, 65pp; English.
XX      The invention relates to the use of an insulin-like growth factor I
XX      (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
XX      of a medicament for treating nerve damage in the peripheral nervous
XX      system, or for treating nerve damage by localising MGF at the site of
XX      damage. The nerve damage may include severing of a nerve. The treatment
XX      may be combined with another treatment (such as a polypeptide growth
XX      factor other than MGF) that prevents or diminishes degeneration of the
XX      target organ (for example, muscle) which the damaged nerve innervates,
XX      whereby the treatment of the muscle with MGF or a polynucleotide encoding
XX      MGF prevents or diminishes degeneration. The method is useful for
XX      treating neurological disorders, preferably motoneuron disorders. These
XX      methods can reduce motoneuron loss by 20% or greater in response to nerve
XX      avulsion. This sequence represents cDNA encoding the human MGF.
XX      Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;
XX      Query Match      89.4%; Score 467.4; DB 24; Length 517;
XX      Best Local Similarity 96.2%; Pred. No. 1,5e-127;
XX      Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;
QY      1 GGACCGGAGACGCTGCGGTGCTGAGCTGAGTGTGATGCTCTTCACTGCTGTGTGAGAC 60
DB      1 GGACCGGAGACGCTGCGGTGCTGAGCTGAGTGTGATGCTCTTCACTGCTGTGTGAGAC 60
QY      61 AGGGGCTTTATTTCACAGACCCACAGATAGGCTCCAGACAGTGGAGGGCACTCTAG 120
DB      61 AGGGGCTTTATTTCACAGACCCACAGATAGGCTCCAGACAGTGGAGGGCACTCTAG 120
QY      121 ACAGGATCGTGATAGTGTCTCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
DB      121 ACAGGATCGTGATAGTGTCTCTTCCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180
QY      181 TTGTCACCCCTCAAGCCGGCAAGGACGCCGCTCCGTCCGTCCAGGCGCACACCCGAC 240
DB      181 TTGTCACCCCTCAAGCCGGCAAGGACGCCGCTCCGTCCGTCCAGGCGCACACCCGAC 240
QY      241 ATGCCCAAGACTCAGAGTATCAGCTCCATCTACCAACAGAAATGAGTCTCAGAG 300
DB      241 ATGCCCAAGACTCAGAGTATCAGCTCCATCTACCAACAGAAATGAGTCTCAGAG 300
QY      301 AGAAGGAAGAGAGTACATTTCAGAAACACAACTAAGAGGAGTGCAGGAACAGACTA 360
DB      301 AGAAGGAAGAGAGTACATTTCAGAAACACAACTAAGAGGAGTGCAGGAACAGACTA 360
QY      298 AGAAGGAAGAGAGTACATTTCAGAAACACAACTAAGAGGAGTGCAGGAACAGACTA 357
DB      298 AGAAGGAAGAGAGTACATTTCAGAAACACAACTAAGAGGAGTGCAGGAACAGACTA 357

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QY      361 CAGCATGTAGAGAACCCCTTCTGAGAGTGAAGAGACAGCCACCGACACCCCTTTG 420
DB      358 CAGGATGTA-GAAGACCCCTTCTGAGAGTGAAGAGGACAGCCACCGACACCCCTTTG 416
QY      421 CTCGTCACAGTTACTCTGTAACATGGAATACCGGCCAAAATAAGTTTATCATCATTT 480
DB      417 CTCGTCACAGTTACTCTGTAACATGGAATACCGGCCAAAATAAGTTTATCATCATTT 476
QY      481 CAAGATGGCATTTCCCAATGAATACACAGTAACAT 521
DB      477 CAAGATGGCATTTCCCAATGAATACACAGTAACAT 517
RESULT 6
AAB06405
ID      AAB06405 standard; cDNA; 471 BP.
XX      AAB06405;
XX      10-AUG-2001 (first entry)
XX      Rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
XX      Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
XX      mechano-growth factor; neurological disorder; neurodegenerative disorder;
XX      amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
XX      poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
XX      nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
XX      sex-linked muscular dystrophy; peripheral neuropathy;
XX      Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.
XX      Oryctolagus cuniculus.
XX      Location/Qualifiers
XX      FT      1..318
XX      CDS      /tag= a
XX      /product= "Liver-type IGF-I isoform (L.IGF-I)"
XX      /transl_except= (pos:7..9, aa:61n)
XX      /note= "These translation exceptions occur while decoding
XX      the alternative version of the protein (AAB02456).
XX      The CDS comprises exons 3, 4 and 6 and
XX      does not include start codon"
XX      FT      WO200136483-A1.
XX      PN      15-NOV-2000; 2000WO-GB04354.
XX      PD      25-MAY-2001.
XX      PF      15-NOV-2000; 2000WO-GB04354.
XX      PR      15-NOV-1999; 99GB-0026968.
XX      PA      (UNLO ) UNIV COLLEGE LONDON.
XX      PI      Goldslink G, Johnson I;
XX      WPI: 2001-355620/37.
XX      P-PSDB: AAE02452, AAE02456.
XX      Use of mechano-growth factor, an isoform of insulin-like Growth
XX      Factor-I, capable of reducing motoneurone loss, in the manufacture of a
XX      medicament for the treatment of neurological disorder.
XX      Disclosure; Page 59-60; 65pp; English.
XX      The present invention relates to use of mechano-growth factor (MGF),
XX      an insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
XX      medicament for the treatment of neurological disorder. The MGF is capable
XX      of reducing motoneurone loss by 20% or greater in response to nerve
XX      avulsion, and effects motoneurone rescue, preferably adult motoneurone
XX      rescue. The MGF polynucleotide and polypeptide are useful in the
XX      manufacture of a medicament for the treatment of a neurological disorder,

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DB 181 TGTGACACCCCTCAAGCCGGCAAGAGCCGCCCTCCCTCCGTCCGCCACAGCCACACCCGAC 240  
QY 241 ATGCCCAAGACTCAGAAAGTATCAGCCCTCCATCTTACCAACAAGAAATGAAGTCTCAGAGG 300  
DB 241 ATGCCCAAGACTCAG----- 255  
QY 301 AGAAGAAAGAGTACATTGGAAGAACACAGTAGAGGGAGTGCAGGAACAAGAACTA 360  
DB 256 -----AAGGAAGTACATTGGAAGAACACAGTAGAGGGAGTGCAGGAACAAGAACTA 308  
QY 361 CAGGATGTAGGAAGACCCCTTCTGAGAGTGAAGAGACAGCCACCGCAGAGACCTTTG 420  
DB 309 CAGGATGTAGGAAGACCCCTTCTGAGAGTGAAGAGACAGCCACCGCAGAGACCTTTG 368  
QY 421 CTCTGCACAGTACCTTACCAATGGAATACCGGCCCAAAATTAAGTTGATCACAATT 480  
DB 369 CTCTGCACAGTACCTTACCAATGGAATACCGGCCCAAAATTAAGTTGATCACAATT 428  
QY 481 CAAAGATGCAATTTCCCAATGAATACACAAGTAACATTC 523  
DB 429 CAAAGATGCAATTTCCCAATGAATACACAAGTAACATTC 471

RESULT 8  
AAB06399  
ID AAB06399 standard; CDNA; 539 BP.

AC AAB06399;

CT 10-AUG-2001 (first entry)

DE Rat IGF-I isoform mechano-growth factor (MGF) cDNA.

XX Rat; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;

KW sex-linked muscular dystrophy; peripheral neuropathy;

KW Alzheimer's disease; Parkinson's disease; ss.

XX Rattus sp.

OS Rattus sp.

XX Key

XX CDS

XX 1..336

XX /tag- a

XX /product= "Mechano-growth factor (MGF)"

XX /note= "This region comprises exons 3-6. The CDS does

XX not include start codon"

XX /partial

XX WO200136483-A1.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000MO-GB04354.

XX 15-NOV-1999; 99GB-0025968.

XX (UNLO ) UNIV COLLEGE LONDON.

XX Goldspink G, Johnson I;

XX WPI; 2001-355620/37.

XX P-PSDB: AAF02448.

XX Use of mechano-growth factor, an isoform of Insulin-like Growth

XX Factor-I, capable of reducing motoneurone loss, in the manufacture of a

XX medicament for the treatment of neurological disorder

XX Claim 4; Page 51-52; 66pp; English.

CC The present invention relates to use of mechano-growth factor (MGF),  
CC an insulin-like Growth factor-I (IGF-I) isoform in the manufacture of a  
CC medicament for the treatment of neurological disorder. The MGF is capable  
CC of reducing motoneurone loss by 20% or greater in response to nerve  
CC avulsion, and effects motoneurone rescue, preferably adult motoneurone  
CC rescue. The MGF polynucleotide and polypeptide are useful in the  
CC manufacture of a medicament for the treatment of a neurological disorder,  
CC including a disorder of motoneurons and/or neurodegenerative disorder,  
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive  
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,  
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a  
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an  
CC injury that affects motoneurons, motoneurone loss associated with aging,  
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,  
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.  
CC The present sequence is rat IGF-I isoform MGF cDNA. MGF is a muscle  
CC isoform having extracellular (EC) domain, hence also referred as  
CC IGF-I-EC. The MGF protein comprises amino acid sequences encoded by  
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame  
CC of MGF.

SO Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

Query Match 68.2%; Score 356.8; DB 22; Length 539;

Best Local Similarity 82.3%; Pred. No. 5.5e-95;

Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

QY 1 GGACCCGAGACCCCTGCGCGTCTGAGCTGAGATGCTCTTCAATTCGTGTGAGAAC 60

DB 1 GGACCCGAGACCCCTGCGCGTCTGAGCTGAGATGCTCTTCAATTCGTGTGAGAAC 60

QY 61 AGGGGCTTTTATTTACAGAGCCACAGAGATAGGCTCCAGAGTGGAGGACACCTCAG 120

DB 61 AGGGGCTTTTATTTACAGAGCCACAGAGATAGGCTCCAGAGTGGAGGACACCTCAG 120

QY 121 AAGGATGCTGATGATGATGCTGCTCCGAGCTGTGATGAGAGGCTGAGATGTAC 180

DB 121 AAGGATGCTGATGATGATGCTGCTCCGAGCTGTGATGAGAGGCTGAGATGTAC 180

QY 122 ACGGCACTTGTGATGATGATGCTGCTCCGAGCTGTGATGAGAGGCTGAGATGTAC 180

DB 122 ACGGCACTTGTGATGATGATGCTGCTCCGAGCTGTGATGAGAGGCTGAGATGTAC 180

QY 181 TGTGACACCCCTCAAGCCGCAAGAGCAGCCGCTCCGCTGCGCAGCCACACCGAC 240

DB 181 TGTGACACCCCTCAAGCCGCAAGAGCAGCCGCTCCGCTGCGCAGCCACACCGAC 240

QY 241 ATGCCCAAGACTCAGAAAGTATCAGCCCTCCATCTACCAACAAGAAATATAGTCTAGAG 300

DB 241 ATGCCCAAGACTCAGAAAGTATCAGCCCTCCATCTACCAACAAGAAATATAGTCTAGAG 300

QY 301 AGAAGAAAGAGTACATTGGAAGAACACAGTAGAGGGAGTGCAGGAACAAGAACTA 360

DB 301 AGAAGAAAGAGTACATTGGAAGAACACAGTAGAGGGAGTGCAGGAACAAGAACTA 360

QY 361 CAGGATGTAGGAAGACCCCTTCTGAGAGTGAAGAGACAGCCACCGCAGAGACCTTTG 420

DB 361 CAGGATGTAGGAAGACCCCTTCTGAGAGTGAAGAGACAGCCACCGCAGAGACCTTTG 420

QY 421 CTCTGCACAGTACCTTACCAATGGAATACCGGCCA-----AAATATAGTTGATC 474

DB 421 CTCTGCACAGTACCTTACCAATGGAATACCGGCCA-----AAATATAGTTGATC 474

QY 475 ACATTTCAGAGAT-GGCAATTCGCCCAATGAATACACAGTAACATTC 523

DB 475 ACATTTCAGAGAT-GGCAATTCGCCCAATGAATACACAGTAACATTC 523

DE Rat mechano-growth factor (MGF) cDNA.

```

XX Rat: mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KM neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KM muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
KM nerve avulsion.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..336
FT     /tag= a
FT     /product= "Rat MGF"
FT     /partial
FT     /note= "No start codon"
FT     1..75
FT     /tag= b
FT     /number= exon 3
FT     76..258
FT     /tag= c
FT     /number= exon 4
FT     259..309
FT     /tag= d
FT     /number= exon 5
FT     310..333
FT     /tag= e
FT     /number= exon 6
XX
XX MO200185781-A2.
XX
XX 15-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-GB02054.
XX
XX 10-MAY-2000; 2000GB-0011278.
XX
XX (UNLO ) UNIV COLLEGE LONDON.
XX PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
XX Goldslink G, Teregnth G;
XX
XX WPI: 2002-055585/07.
XX P-PSDB: AA010560.
XX
XX Use of insulin-like growth factor I (IGF-I) isoform known as
XX mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
XX ability to reduce motoneuron loss in response to nerve avulsion, to
XX treat nerve damage
XX
XX Disclosure: Fig 6: 65pp; English.
XX
XX The invention relates to the use of an insulin-like growth factor I
XX (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
XX of a medicament for treating nerve damage in the peripheral nervous
XX system, or for treating nerve damage by localising MGF at the site of
XX damage. The nerve damage may include severing of a nerve. The treatment
XX may be combined with another treatment (such as a polypeptide growth
XX factor other than MGF) that prevents or diminishes degeneration of the
XX target organ (for example, muscle) which the damaged nerve innervates.
XX whereby the treatment of the muscle with MGF or a polynucleotide encoding
XX MGF prevents or diminishes degeneration. The method is useful for
XX treating neurological disorders, preferably motoneuron disorders. These
XX methods can reduce motoneuron loss by 20% or greater in response to nerve
XX avulsion. This sequence represents cDNA encoding the rat MGF.
XX
XX Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other:
XX
Query Match 68.2%; Score 356.8; DB 24; Length 539;
Best Local Similarity 82.3%; Pred. No. 5,5e-95;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;
QY 1 GGACCGAGACGCGCTGCGGCTGCTGAGCTGAGTGCCTTCCTTCAGTGTGTGAGAC 60
DB 1 GGACCGAGACGCGCTTGGCGGCGCTGAGCTGAGTGCCTTCCTTCAGTGTGTGAGAC 60

```

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QY 61 AGGCGCTTTATTTCACCAAGCCCAAGATACGCGCTCCAGCATGTGGAGGCGACTCG 120
DB 61 AGGCGCTTTATTTCACCAAGCCCAAGATACGCGCTCCAGCATGTGGAGGCGACTCG 120
QY 121 ACAGCATCGTGGATGAGTGTCTGCTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 180
DB 121 ACAGCATCGTGGATGAGTGTCTGCTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 180
QY 181 TGTGCACCCCTCAAGCCGCGAAGAGCAGCCGCTCCGTCCTCCAGCCGACACCGAC 240
DB 181 TGTGCACCCCTCAAGCCGCGAAGAGCAGCCGCTCCGTCCTCCAGCCGACACCGAC 240
QY 241 ATGCCCAAGACTGAGATATCAGCCCTCCATCTTACCAAGAAATGAGTGTGAGAG 300
DB 241 ATGCCCAAGACTGAGATATCAGCCCTCCATCTTACCAAGAAATGAGTGTGAGAG 300
QY 301 AGAAGAAAGAAAGTACATTTGAAGAACAAGTAGAGGAGTGCAGAAACAGAACTA 360
DB 301 AGAAGAAAGAAAGTACATTTGAAGAACAAGTAGAGGAGTGCAGAAACAGAACTA 360
QY 361 CAGATGTAGAGAGACCTCTGAGGAGTGAAGAAGACAGCGCCAGACGACCTTTG 420
DB 361 CAGATGTAGAGAGACCTCTGAGGAGTGAAGAAGACAGCGCCAGACGACCTTTG 420
QY 421 CTCTGCACAGTACCTGTAAACATTTGGAATACCGGCA-----AAAAATACTTGATC 474
DB 421 CTCTGCACAGTACCTGTAAACATTTGGAATACCGGCA-----AAAAATACTTGATC 474
QY 475 ACATTTCAAGAT-GGCAATTTCCCGCCATGAAATACCAAGTAAACATTC 523
DB 475 ACATTTCAAGAT-GGCAATTTCCCGCCATGAAATACCAAGTAAACATTC 523
QY 481 TCATTTGAGAGATGGGCAATTTCCCTCAATGAAATACCAAGTAAACATTC 530
DB 481 TCATTTGAGAGATGGGCAATTTCCCTCAATGAAATACCAAGTAAACATTC 530

RESULT 10
AAAT0436
ID AAAT0436 standard; cDNA; 818 BP.
XX
XX AC AAAT0436;
XX
XX 05-APR-1991 (first entry)
XX
XX Sequence encoding Insulin-like growth factor 1A (IGF-1A).
XX
XX Growth promoter; lactation enhancer; cell proliferation; ss.
XX
XX Homo sapiens.
XX
XX EP229750-A.
XX
XX 22-JUL-1987.
XX
XX 06-JAN-1987; 87EP-0870001.
XX
XX 20-NOV-1986; 86US-0929671.
XX
XX 07-JAN-1986; 86US-0816662.
XX
XX (UNIM ) UNIV OF WASHINGTON.
XX
XX Kriegl G, Rotwein PS;
XX
XX WPI: 1987-200203/29.
XX
XX New pre-pro-insulin-like growth factor-1 protein - obid. by
XX recombinant DNA procedures for use as growth promoters for
XX enhancing lactation, for stimulating cell proliferation etc.
XX
XX Example; Fig 5; 59pp; English.
XX
XX A 42 base oligonucleotide corresponding to the DNA sequence encoding
XX amino acids 10 to 23 of mature human IGF-1 was synthesized (AAAT0437).
XX The radiolabeled 42 mer was then employed to screen for IGF-1
XX containing DNA sequences in a human liver cDNA library. Insulin-

```

CC 1 like growth factors-1A and -1B cDNAs were isolated from a human cDNA  
 CC library by using lambdaBst 11 (AAN70435, AAN70436). The human IGF-1  
 CC genomic gene was isolated and mapped. It encodes at least two  
 CC preproinsulin-like growth factor-1 proteins. An essentially pure  
 CC preproinsulin-like growth factor-1 protein comprising the sequence  
 CC of amino acids shown in Figure six is claimed (AAP70277).

XX Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other:

Query Match 63.9%; Score 334.4; DB 8; Length 818;  
 Best Local Similarity 84.6%; Pred. No. 2.6e-88;  
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

QY 1 GGACCGGAGACGCTGCTGGCTGCTGAGAGCTGGAGAGCTCTTCAGTTCGTGTGAGAGAC 60  
 DB 203 GGACCGGAGACGCTGCTGGCTGCTGAGAGCTGGAGAGCTCTTCAGTTCGTGTGAGAGAC 262  
 QY 61 AGGGGCTTTTATTTCACACAGCCACAGATACGGCTCCAGCAGTGAGAGGACCTCAG 120  
 DB 263 AGGGGCTTTTATTTCACACAGCCACAGATACGGCTCCAGCAGTGAGAGGACCTCAG 322  
 QY 121 ACAGGATCGTGTGATGATGCTGCTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 180  
 DB 323 ACAGGATCGTGTGATGATGCTGCTCCGAGCTGTGATGTGAGAGGCTGAGATGTAT 382  
 QY 181 TGTGCACCCCTCAAGCCGCAAGGACCCGCTCCGCTCCGACAGCCACACCGAC 240  
 DB 383 TGGCCACCCCTCAAGCCGCAAGGACCCGCTCCGCTCCGACAGCCACACCGAC 442  
 QY 241 ATGCCCAAGACTCGAGATATCAGCCCTCCTATACACAGAAATGAAGTTCAGAGG 300  
 DB 443 ATGCCCAAGACTCGAGATATCAGCCCTCCTATACACAGAAATGAAGTTCAGAGG 457  
 QY 301 AGAAGGAAGGAAGTACATTGAAGAACACAGTACAGAGGAGTGCAGAGAAACAGACTA 360  
 DB 458 -----AAGGAAGTACATTGAAGAACACAGTACAGAGGAGTGCAGAGAAACAGACTA 510  
 QY 361 CAGGATGTAGGAAGACCTCTGTGAGAGTGAAGAGACAGCCACCGACGACCTTGG 420  
 DB 511 CAGGATGTAGGAAGACCTCTGTGAGAGTGAAGAGTACATGACACGCGAGATCCTTGG 570  
 QY 421 CTCTGCAC-AGTACCTG-TAAACATTTGAATACCGGCCCAAAAAATTAAGTTGATCAGAT 478  
 DB 571 CTCTGCACAGATACCTGTTAACTTTGAACACTTGAACACTTGAACAAATTAAGTTGATCAGAT 630  
 QY 479 TTCAAAGAT-GGCATTTCCCCCAATGAATACACAGTAAACATTC 523  
 DB 631 TTCAAAGATGGGCTTTCCCCCAATGAATACACAGTAAACATTC 676

RESULT 11  
 ABR84583  
 ID ABR84583 standard; cDNA; 7260 BP.

XX ABR84583;

XX 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #1154.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;  
 KW vital infection; parasitic infection; protozoal infection;  
 KW fungal infection; sterile inflammatory disease; psoriasis;  
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KW adult respiratory distress syndrome; inflammatory bowel disease;  
 KW Crohn's disease; ulcerative colitis; periodontal disease;  
 KW granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

XX MO200228999-A2.

XX

PD 11-APR-2002.

XX 03-OCT-2001; 2001MO-US30821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

PT Detecting granulocyte activation by detecting differential expression  
 PT of genes associated with granulocyte activation, which serves as  
 PT diagnostic markers that is useful for monitoring disease states and  
 PT drug toxicity

PS Claim 1; SEQ ID No 1154; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation  
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
 CC DNA chip analysis as given in the specification, and comparing  
 CC the expression level to an expression level in an unactivated  
 CC GC, where differential expression of Gs is indicative of GCA.  
 CC Also included are modulating (M2) GA by contacting GC with an agent  
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)  
 CC for an agent capable of modulating GCA or an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease using the  
 CC gene expression profile; (3) detecting (M4) an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease, by detecting the  
 CC level of expression in a sample of the tissue of gene(s) from Gs, where  
 CC the level of expression of the gene is indicative of inflammation;  
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,  
 CC an allergic response in a subject, exposure of a subject to a pathogen  
 CC or sterile inflammatory disease, by contacting a tissue having  
 CC inflammation with an agent that modulates the expression of gene(s)  
 CC from Gs in the tissue. M1 is useful for detecting GCA. M2 is useful for  
 CC modulating GA; M3 is useful for screening an agent capable of modulating  
 CC GCA preferably in an inflammation in a tissue; M4 is useful for  
 CC detecting an inflammation (especially chronic) in a tissue, an allergic  
 CC response in a subject, exposure of a subject to a pathogen or sterile  
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal  
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC periodontal disease; also bacterial infection, viral infection,  
 CC parasitic infection, protozoal infection, fungal infection and M5 is  
 CC useful for treating one of the above conditions. The present  
 CC sequence represents a gene differentially expressed in granulocytes.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other:

Query Match 63.9%; Score 334.4; DB 24; Length 7260;  
 Best Local Similarity 84.6%; Pred. No. 6.1e-88;  
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

QY 1 GGACCGGAGACGCTGCTGGCTGCTGAGAGCTGGAGAGCTCTTCAGTTCGTGTGAGAGAC 60  
 DB 311 GGACCGGAGACGCTGCTGGCTGCTGAGAGCTGGAGAGCTCTTCAGTTCGTGTGAGAGAC 370  
 QY 61 AGGGGCTTTTATTTCACACAGCCACAGATACGGCTCCAGAGCTGCGAGGCGACTCAG 120  
 DB 371 AGGGGCTTTTATTTCACACAGCCACAGATACGGCTCCAGAGCTGCGAGGCGCGCTCAG 430  
 QY 121 ACAGGATCGTGTGATGATGCTGCTCCGAGCTGTGATGTGAGAGGCTGAGATGTAC 180  
 DB 431 ACAGGATCGTGTGATGATGCTGCTCCGAGCTGTGATGTGAGAGGCTGAGATGTAT 490

Oy	181	TGCGACCCCTCAAGCGGGCAAGGACGCCGCTCCGCTGCTGCGACGCGCAACCGAC	240
Oy	491	TGGCAGCCCTCAAGCCTGCCAAGTCAGCTGCTGTGCTGTCCGACGCGCACCGAC	550
Oy	241	ATGCCCCAGACTCAGAGTATCAGCCTCATCTACCAAGAAATGAAATCTCAGAG	300
Db	551	ATGCCCCAAGCCCG-----565	
Oy	301	AGAAGAAAGAGTCACTTTGAGACACAGTAGTAGGAGTGCAGGAAACAGAACTA	360
Db	566	-----AAGAGATCACTTTGAGACGCCAGTAGTAGGAGTGCAGGAAACAGAACTA	618
Oy	361	CAGAGTGTAGGAAGACCCCTTCTGAGAGTGAAGAAAGACAGGCCACCGACGCCCTTTG	420
Db	619	CAGAGTGTAGGAAGACCCCTCTGAGAGTGAAGAAAGTGCATGACCGCACGATCCTTG	678
Oy	421	CTGTGCAAC-AGTACCTG-TAAACAATGGAATACGGCGCAAAAAATAGTTTGATCAT	478
Db	679	CTGTGCAAGATTAAGTCTGTTAAACTTTGGAACCACTACCAAAAAATAGTTTGATCAT	738
Oy	479	TTCGAAGAT-GGCATTTTCCCCCAATGAATATACACAGTAACCATTC	523
Db	739	TTCGAAGATGGGCGTTTCCCCCAATGAATATACACAGTAACCATTC	784

RESULT 12  
 ID ABN97244 standard; DNA: 7260 bp.  
 XX ABN97244;  
 AC  
 XX  
 XX ABN97244;  
 DT 13-AUG-2002 (first entry)  
 XX  
 DE Gene #3742 used to diagnose liver cancer.  
 XX  
 KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;  
 KW metastatic liver tumour; cytostatic; expression profile; disease state;  
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200229103-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 02-OCT-2001; 2001WO-US030589.  
 XX  
 PR 02-OCT-2000; 2000US-237054P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;  
 XX  
 DR WPI; 2002-426119/45.  
 XX  
 PR Diagnosing and detecting the progression of liver cancer.  
 PR hepatocellular carcinoma or metastatic liver tumor in a patient,  
 PR involves detecting the level of expression of two or more genes in a  
 PR liver tissue sample  
 XX  
 PS Claim 1; SEQ ID NO 3742; 298bp; English.  
 XX  
 CC The invention relates to a novel method for diagnosing and detecting the  
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver  
 CC tumour in a patient, and differentiating metastatic liver cancer from  
 CC hepatocellular carcinoma in a patient, involving detecting the level of  
 CC expression of two or more genes represented in ABN93503-ABN97455 in a  
 CC tissue sample. The method of the invention has hepatotropic, and  
 CC cytostatic activity. The method is useful for diagnosing and detecting  
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic  
 CC liver carcinoma in a patient. The method is useful for identifying,  
 CC expression profiles which serve as useful diagnostic markers as well as

CC markers that can be used to monitor disease status, disease progression,  
CC drug toxicity, drug efficacy and drug metabolism.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp://wipo.int/pub/pubinfo/seq\\_pcr\\_sequences](http://wipo.int/pub/pubinfo/seq_pcr_sequences).  
XX  
XX Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match	63.9%	Score 334.4;	DB 24;	Length 7260;
Best Local Similarity	84.6%	Pred. No. 6.1e-88;		
Matches 445;	Conservative	0;	Mismatches 26;	Indels 55;
				Gaps 4;

QY	1	GGACCGSAGAGCGCTCTGGCGGTCGTAGTGTGGATGTCTTCAATGCTGTGTGGAGAC	60
Db	311	GGACCGSAGAGCGCTCTGGCGGTCGTAGTGTGGATGTCTTCAATGCTGTGTGGAGAC	370
QY	61	AGGGGCTTTTATTTCAACAAGCCCAAGATACGGCTCCACAGCTCGSAGGSCACCTCAG	120
Db	371	AGGGGCTTTTATTTCAACAAGCCCAAGATACGGCTCCACAGCTCGSAGGSCCTCAG	430
QY	121	ACAGGCATCGTGGATGAGTGTGCTGTCCGGAGCTGTGATCTGAGGAGGCTGTGACATGAC	180
Db	431	ACAGGCATCGTGGATGAGTGTGCTGTCCGGAGCTGTGATCTGAGGAGGCTGTGAGTGTAT	490
QY	181	TGTGACCCCTTCACAAACCCGCAAAAGGACACCCGCTCTCGTCGTCGCCACGCGCACCCGAC	240
Db	491	TGCGACCCCTTCACAAACCCGCTCGCCAAAGTCAGCTGTGCTGTGCGGACACGCGCACCCGAC	550
QY	241	ATGCCCAAGACTCAGAAAGTATCAGCCTCCATCTACCAACAAGAAATGAAGTCTCAGAG	300
Db	551	ATGCCCAAGACCCCA-----	565
QY	301	AGAAAGGAAGGAGTACATTTGAAGAACACAGTAGSAGGAGTGCGAGSAAACAAGAACTA	360
Db	566	-----AAGSAGTACATTTGAAGAACACGAAGTAGAGGAGTGGAGSAAACAAGAACTA	618
QY	361	CAGATGTAGGAAGACCCTTCTGAGAGATGAAGAAGACAGGCCACCCGACAGACCTTTG	420
Db	619	CAGSAGTGTAGGAAGACCCTCTCTGAGAGATGAAGATGTGACATGCCACCCGACAGATCTTTG	678
QY	421	CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCAAAAATAAGTTGATCATAT	478
Db	679	CTCTGCACAGATTACTCTTAAACTTTGGAACACCTTACCAAAAATAAGTTTGAATACAT	738
QY	479	TTCAAGAT-GGCAATTTCCCCAATGAATAACAGATGAATTC	523
Db	739	TTAAAGATGGCGCTTCTCCCAAGAAATACACAGTAATCATTC	784

RESULT 13  
ABR64812  
ID ABR64812 standard; DNA; 7260 BP.  
XX  
AC ABR64812;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Human benign prostatic hyperplasia gene #707.  
XX  
KM Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN W020021244-0-A2.  
XX  
XS 14-FEB-2002.  
PD  
XX  
PF 07-AUG-2001; 2001WO-US24708.  
XX  
XX  
PR 07-AUG-2000; 2000US-223323P.  
PR 05-JUN-2001; 2001US-0873519.  
XX  
PA (GENE-). GENE LOGIC INC.

PA (NISE ) JAPAN TOBACCO INC.

PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;

DR WPI: 2002-257476/30.

PT identifying drugs for and diagnosing benign prostatic hyperplasia, by PT detecting expression levels of one or more genes in prostate cells from PT patient that are differentially regulated compared to normal prostate PT cells -

PS Disclosure; Page 391-393; 444pp; English.

CC The invention relates to a method of diagnosing (I) the onset or  
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for  
CC or identifying an agent that modulates the onset or progression of BPH.  
CC The method is based on changes in gene expression in BPH tissue isolated  
CC from patients exhibiting different clinical states of prostate  
CC hyperplasia as compared to normal prostate tissue. (I) comprises  
CC detecting the expression levels of one or more genes in prostate cells  
CC from the subject that are differentially regulated compared to normal  
CC prostate cells. (II) comprises preparing a first gene expression profile  
CC of BPH cells or BPH-like cell population, exposing the cells to the  
CC agent, preparing a second gene expression profile of the agent exposed  
CC cells, and comparing the first and second gene expression profiles.  
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is  
CC useful for identifying an agent that modulates the onset or progression  
CC of BPH. The methods are useful to present information identifying  
CC the expression level in a tissue or cells, by comparing the expression  
CC level of genes given in the specification in the tissue or cells to the  
CC level of expression of gene in the database, and displaying the  
CC expression levels of at least one gene in the tissue or cell sample  
CC compared to the expression level in BPH. Agents using (II) are useful for  
CC treating BPH or prostate cancer. ABK4106-ABK4860 represent human  
CC benign prostatic hyperplasia gene sequences of the invention.

Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match	Score	DB	Length
63.98;	334.4;	24;	7260;

Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

[illegible]

QY      479 TTCAAGAT-GGCATTCCCCCATGAATACCAAGTAACATTC 523  
         || ||||| || | ||||| ||||| ||||| ||||| |||||  
Db      739 TTTAAAGATGGCGTTCCTCCCATGAAATACCAAGTAACATTC 784

RESULT 14  
ABK35504  
ID ABK35504 standard; DNA; 7260 BP

The invention relates to diagnosing endometrial cancer in a subject suspected of having endometrial cancer comprising determining the expression of a set of nucleic acid molecules or expression products in an endometrial sample suspected of being cancerous, where the set of nucleic acid molecules comprises at least 2 nucleic acid molecules selected from 50 fully defined sequences as given in the specification. The nucleic acids are used as an array of at least 2 of the 50 nucleic acids bound to a solid substrate. Also included is a solid-phase protein microarray comprising at least 2 antibodies or its antigen binding fragments, that specifically bind at least 2 different polypeptides from the 50 fully defined sequences as given in the specification, fixed to a solid substrate. The methods and arrays are useful for the diagnosis of endometrial cancer, selecting and monitoring treatment regimens and identification of lead compounds useful for the treatment of endometrial cancer. The present sequence is one of 50 genes differentially expressed between cancerous and non-cancerous samples.

Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other

Query Match	63.9%	Score 134.4;	DB 24;	Length 7260;
Best Local Similarity	84.6%;	Pred. No. 6.1e-88;		
Matches 445; Conservative	0;	Mismatches 26;	Indels 55;	Gaps 4;

QY	1	GSACCCGAGACGGCTCGCGCGCTGCTGAGCTGGTGGATGCTTCAAGTGGTGTGGAGAC	60
Db	311	GSACCCGAGACGCTCGCGCGGCTGAGCTGGTGGATGCTCTTCAAGTGGTGTGGAGAC	3707
QY	61	AGGGGCTTTAATTCACAACGCCACAGAGATACGGCTCCAGACGTGGAGGGCACTCCAG	120
Db	371	AGGGGCTTTAATTCACAACGCCACAGGGTATGGCTCCACACAGTGGAGGGGCCCTCCAG	430



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OK nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:46:38 ; Search time 42.3965 Seconds  
(without alignments)  
3783.145 Million cell updates/sec

Title: US-09-852-261-5

Perfect score: 523

Sequence: 1 ggaacgagagcgtctgcg.....aaatacaagaataacattc 523

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*

2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*

4: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*

5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	100.0	553	4	US-09-142-583A-3
2	523	100.0	553	4	US-09-142-583A-5
3	332.8	63.6	777	4	US-09-142-583A-10
4	331.2	63.3	622	6	5405942-2
5	274.6	52.5	5707	2	US-08-472-809B-8
6	274.6	52.5	6345	2	US-08-472-809B-7
7	234.4	44.8	357	6	5405942-13
8	232.8	44.5	357	6	5405942-9
9	191.4	36.6	210	6	5405942-11
10	191.4	36.6	210	6	5405942-11
11	191.4	36.6	210	6	5405942-11
12	189.8	36.3	210	6	5405942-15
13	185.2	35.4	240	5	US-08-308-196A-1
14	185.2	35.4	240	5	PCT-US91-06452-1
15	185.2	35.4	390	3	US-09-029-267-13
16	158.8	30.4	798	1	US-07-953-230A-6
17	154.8	29.6	846	1	US-07-953-230A-1
18	154.8	29.6	846	1	US-07-953-230A-5
19	127	24.3	621	3	US-08-989-251-40
20	127	24.3	621	3	US-08-989-251-40
21	127	24.3	621	3	US-08-989-251-40
22	125.8	24.1	233	1	US-08-444-142-3
23	125.8	24.1	233	1	US-08-444-142-3
24	125.8	24.1	485	1	US-07-989-845-29
25	125.8	24.1	485	1	US-07-989-845-29
26	125.8	24.1	485	1	US-08-110-663-1
27	125.8	24.1	485	1	US-08-169-686-1

28	125.8	24.1	485	1	US-08-240-121-13	Sequence 13, Appl
29	125.8	24.1	485	1	US-08-451-241-13	Sequence 13, Appl
30	125.8	24.1	485	1	US-08-110-664-1	Sequence 1, Appl
31	125.8	24.1	485	1	US-08-446-882-1	Sequence 1, Appl
32	125.8	24.1	485	1	US-08-385-187A-1	Sequence 1, Appl
33	125.8	24.1	485	1	US-08-470-108-1	Sequence 1, Appl
34	125.8	24.1	485	5	PCT-US93-11297-13	Sequence 29, Appl
35	125.8	24.1	485	5	PCT-US93-11298-29	Sequence 29, Appl
36	125.6	24.0	243	2	US-08-482-182-75	Sequence 75, Appl
37	124.2	23.7	717	1	US-08-284-784-40	Sequence 40, Appl
38	124.2	23.7	717	2	US-08-854-811-40	Sequence 40, Appl
39	124.2	23.7	783	1	US-08-284-784-43	Sequence 43, Appl
40	124.2	23.7	783	2	US-08-854-811-43	Sequence 43, Appl
41	124.2	23.7	891	1	US-08-284-784-33	Sequence 33, Appl
42	124.2	23.7	891	1	US-08-284-784-34	Sequence 34, Appl
43	124.2	23.7	891	2	US-08-854-811-33	Sequence 33, Appl
44	124.2	23.7	891	2	US-08-854-811-34	Sequence 34, Appl
45	124.2	23.7	900	1	US-08-284-784-24	Sequence 24, Appl

## ALIGNMENTS

RESULT 1  
US-09-142-583A-3  
Sequence 3, Appl  
Patent No. 6221842  
GENERAL INFORMATION:  
APPLICANT: GOLDSPIK, GEOFFREY  
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P. C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/142,583A  
FILING DATE: 29-Oct-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB97/00658  
FILING DATE: 11-MAR-1997  
APPLICATION NUMBER: GB 9605124.8  
FILING DATE: 11-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B. J.  
REGISTRATION NUMBER: 36663  
REFERENCE/DOCKET NUMBER: 117-263  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..363  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-142-583A-3  
Query Match 100.0%; Score 523; DB 4; Length 553;

QY	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTAAATTGTTGTTGTTGAGAC	60
Db	31	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTAAATTGTTGTTGTTGAGAC	90
QY	61	AGGGGCTTTATTTTAAACAAGCCACAGAGATAGCGCTCCAGCAGTGGAGGGGACCTTCAG	120
Db	91	AGGGGCTTTATTTTAAACAAGCCACAGAGATAGCGCTCCAGCAGTGGAGGGGACCTTCAG	150
QY	121	ACAGGATGCTGGATGATGATGCTGCTTCGCGAGCTGTGATTTGAGAGGCTGGAGATGAC	180
Db	151	ACAGGATGCTGGATGATGATGCTGCTTCGCGAGCTGTGATTTGAGAGGCTGGAGATGAC	210
QY	181	TGTGACCCCTTAAACCCGGCAAAAGGACGCGCTCCGTCGTCGCCAGCGCCACACCGAC	240
Db	211	TGTGACCCCTTAAACCCGGCAAAAGGACGCGCTCCGTCGTCGCCAGCGCCACACCGAC	270
QY	241	ATGCCCAACATCCAAATATACGCTTCATCTACCAAGAATAATGAAGTCTCAGAG	300
Db	271	ATGCCCAACATCCAAATATACGCTTCATCTACCAAGAATAATGAAGTCTCAGAG	330
QY	301	AGAGAGAAAGGAAGTACATTTGAAGAACACACAAGTAGAGGAGTGCAGAGAAACAGAACTA	360
Db	331	AGAGAGAAAGGAAGTACATTTGAAGAACACACAAGTAGAGGAGTGCAGAGAAACAGAACTA	390
QY	361	CAGAGATGAGAAAGACCTCTCGAGAGATGAAGAGACAGCGCCAGGACCGACCTTTG	420
Db	391	CAGAGATGAGAAAGACCTCTCGAGAGATGAAGAGAGACAGCGCCAGGACCGACCTTTG	450
QY	421	CTCTGCACAGTTACTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATACATT	480
Db	451	CTCTGCACAGTTACTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATACATT	510
QY	481	CAAGATGGCATTTCCCCCAATGAATAACAAAGTAACATTTC	523
Db	511	CAAGATGGCATTTCCCCCAATGAATAACAAAGTAACATTTC	553

RESULT 2  
 US-09-142-583A-5  
 : Sequence 5, Application US/09142583A  
 : Patent No. 6221842  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: GOLDSPIK, GEORFFREY  
 :  
 : TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS  
 :  
 : NUMBER OF SEQUENCES: 11  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: NIXON & VANDERHVE P.C.  
 : STREET: 1100 NORTH GLEBE ROAD  
 : CITY: ARLINGTON  
 : STATE: VA  
 : COUNTRY: USA  
 : ZIP: 22201  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent Release #1.0, Version #1.25  
 :  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/142,583A  
 : FILING DATE: 29-OCT-1998  
 : CLASSIFICATION: <Unknown>  
 :  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: WO PCT/CB97/00658  
 : FILING DATE: 11-MAR-1997  
 : APPLICATION NUMBER: GB 9605124.8  
 : FILING DATE: 11-MAR-1996  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: SADOFF, B. J.  
 : REGISTRATION NUMBER: 36663  
 : REFERENCE/DOCKET NUMBER: 117-263

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 341..397
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-142-583A-5

Query Match          100.0%; Score 523; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 1,38-154;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGACCGAGACGCTCTGCGTGCTGAGCTGTGGATGCTTTCAGTTGCTGTGTGGAGAC   60
DB      31 GGACCGGAGAGCGCTCTGCGTGCTGTGAGTGTGGATGCTTTCAGTTGCTGTGTGGAGAC   90
QY      61 AGGGGCTTTATTTCACAACGCCACAGAAATACGGACTCCACAGTCGAGGAGGCACCCTCAG   120
DB      91 AGGGGCTTTATTTCACAACGCCACAGAAATACGGCTCCACAGTCGAGGAGGCACCCTCAG   150
QY      121 ACAGGCAATCGTGATGAATGCTGCTTCCGGAGCTGTATCTTGAGGAGGCTGGAGATGTAC   180
DB      151 ACAGGCAATCGTGAGATGATGCTGCTTCCGGAGCTGTATCTTGAGGAGGCTGGAGATGTAC   210
QY      181 TGTGACCCCTCCAAGCCGCAAAGGACGCCGCTCGTCCGTGCCACAGCCGACACCGCAC   240
DB      211 TGTGACCCCTCCAAGCCGCAAAGGACGCCGCTCGTCCGTGCCACAGCCGACACCGCAC   270
QY      241 ATGCCCAAGACTCAGAABATATCAGCTCATCTTACCAACAGAATAATTAAGTCTCAGAG   300
DB      271 ATGCCCAAGACTCAGAABATATCAGCTCATCTTACCAACAGAATAATTAAGTCTCAGAG   330
QY      301 AGAAGGAAGAAGATACATTGTAAGAACACAACTAGTAGAGGAGTGCAGAGAAACAAAGACTA   360
DB      331 AGAAGGAAGAAGATACATTGTAAGAACACAACTAGTAGAGGAGTGCAGAGAAACAAAGACTA   390
QY      361 CAGATGTAGAGAAACCTTCTGAGAGATGAAAGAGACAGGCCACCCGAGACCCCTTTG   420
DB      391 CAGATGTAGAGAAACCTTCTGAGAGATGAAAGAGACAGGCCACCCGAGACCCCTTTG   450
QY      421 CTCTGCACAGTACCTGTAAACATTTGGAATACCGGCCCAAAAAATTAAGTTTGCATCATTT   480
DB      451 CTCTGCACAGTACCTGTAAACATTTGGAATACCGGCCCAAAAAATTAAGTTTGCATCATTT   510
QY      481 CAAGATGGCATTTCCCCCAATGAATACACAAGTAACATTC   523
DB      511 CAAGATGGCATTTCCCCCAATGAATACACAAGTAACATTC   553

RESULT 3
US-09-142-583A-10
Sequence 10, Application us/09142583A
Patent No. 6221842
GENERAL INFORMATION:
APPLICANT: GOLDSPIK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESS: NIXON & VANDERHUYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/142,583A  
FILING DATE: 29-Oct-1998  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB97/00658  
FILING DATE: 11-MAR-1997  
APPLICATION NUMBER: GB 9605124.8  
FILING DATE: 11-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B. J.  
REGISTRATION NUMBER: 36663  
REFERENCE/DOCKET NUMBER: 117-263  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
FAX: 7038164100  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 777 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 26..493  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-142-583A-10  
Query Match  
Best Local Similarity 84.4%; Pred. No. 7.7e-95;  
Matches 444; Conservative 0; Mismatches 27; Indels 55; Gaps 4;  
1 GGACCGGAGACGCTCTGCGTGTGAGTGTGATCTTCAAGTTCGTTGTGTGAGAC 60  
179 GGACCGGAGACGCTCTGCGTGTGAGTGTGATCTTCAAGTTCGTTGTGTGAGAC 228  
61 AGGGGCTTTATTTCAACAAGCCACAGATAGCGCTCCAGAGTGGAGGCGACCTCAG 120  
239 AGGGGCTTTATTTCAACAAGCCACAGAGTATGCTCCAGAGTGGAGGCGCTCAG 298  
121 ACAAGCATCTGTGATGATGCTGCTTCCGAGCTGTATCTAGAGAGCTGTGAGATGTAC 180  
299 ACAAGTATCTGTGATGATGCTGCTTCCGAGCTGTATCTAGAGAGCTGTGAGATGTAT 358  
181 TGTGACACCCCTCAAGCGGCAAAAGGACGCTCCGCTGCGGCGCCAGCCACACCGAC 240  
359 TGGGACCCCTCAAGCGCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 418  
241 ATGCCCAAGACTCAAGATGATCAAGCTCTCATCTACCAAGAAATGAAGTCTCAGAGG 300  
419 ATGCCCAAGACTCAAGATGATCAAGCTCTCATCTACCAAGAAATGAAGTCTCAGAGG 433  
301 AGAAGAAAGAAAGTATGTAAGAACACAAAGTAGAGGAGTGCAGAAACAAAGACTA 360  
434 -----AAGAAAGTATGTAAGAACACAAAGTAGAGGAGTGCAGAAACAAAGACTA 486  
361 CAGGATGTAGAAAGACCTTCTGAGAGTGAAGAAGAGACGCGCAGCGACCTTTG 420  
487 CAGGATGTAGAAAGACCTTCTGAGAGTGAAGAAGAGACGCGCAGCGACCTTTG 546  
421 CTCTGCAC-AGTACCTG-TAAACATGSAATACCGGCCCAAAATAGTTTATCATCAT 478  
547 CTCTGCACGAGTACCTGTTAACTTTGAAACACCTTCCAAAAATAGTTTATCATCAT 606  
479 TTCAAAGAT-GGCATTTCCCAATGAATACACAAAGTAAACATTC 523  
607 TTAAAGATGGCGCTTTCCCAATGAATACACAAAGTAAACATTC 652

RESULT 4  
5405942-2  
Patent No. 5405942  
APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER, JAMES P.  
TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS  
I AND II  
NUMBER OF SEQUENCES: 16  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/65,673  
FILING DATE: 16-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 630,557  
FILING DATE: 19-JUL-1984  
SEQ ID NO: 2:  
LENGTH: 622  
5405942-2  
Query Match  
Best Local Similarity 68.3%; Pred. No. 2.2e-94;  
Matches 359; Conservative 84; Mismatches 28; Indels 55; Gaps 4;  
1 GGACCGGAGACGCTCTGCGTGTGAGTGTGATCTTCAAGTTCGTTGTGTGAGAC 60  
45 GGACCGGAGACGCTCTGCGTGTGAGTGTGATCTTCAAGTTCGTTGTGTGAGAC 104  
61 AGGGGCTTTATTTCAACAAGCCACAGATAGCGCTCCAGAGTGGAGGCGACCTCAG 120  
105 AGGGGCTTTATTTCAACAAGCCACAGATAGCGCTCCAGAGTGGAGGCGACCTCAG 164  
121 ACAAGCATCTGTGATGATGCTGCTTCCGAGCTGTATCTAGAGAGCTGTGAGATGTAC 180  
165 ACAAGTATCTGTGATGATGCTGCTTCCGAGCTGTATCTAGAGAGCTGTGAGATGTAT 224  
181 TGTGACACCCCTCAAGCGGCAAAAGGACGCTCCGCTGCGGCGCCAGCCACACCGAC 240  
225 TGGGACCCCTCAAGCGCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 284  
241 ATGCCCAAGACTCAAGATGATCAAGCTCTCATCTACCAAGAAATGAAGTCTCAGAGG 300  
285 AUGCCCAAGACCCAG----- 299  
301 AGAAGAAAGAAAGTATGTAAGAACACAAAGTAGAGGAGTGCAGAAACAAAGACTA 360  
300 -----AAGAAAGTATGTAAGAACACAAAGTAGAGGAGTGCAGAAACAAAGACTA 352  
361 CAGGATGTAGAAAGACCTTCTGAGAGTGAAGAAGAGACGCGCAGCGACCTTTG 420  
353 CAGGATGTAGAAAGACCTTCTGAGAGTGAAGAAGAGACGCGCAGCGACCTTTG 412  
421 CTCTGCAC-AGTACCTG-TAAACATGSAATACCGGCCCAAAATAGTTTATCATCAT 478  
413 CUCUGCAGAGUACUCUGUAAACUUGGAAACUCCCAAAAUAAUAAUUGUAAUAAUUG 472  
479 TTCAAAGAT-GGCATTTCCCAATGAATACACAAAGTAAACATTC 523  
473 UUAAGAAGUUGGCGUUCUCCCAAGAAUUAACAAAGUAAAUU 518  
RESULT 5  
US-08-472-809B-8  
Sequence 8, Application US/08472809B  
Patent No. 5925564  
GENERAL INFORMATION:  
APPLICANT: Schwartz, Robert J.  
APPLICANT: Demayo, Franco J.  
APPLICANT: O'Malley, Bert W.  
TITLE OF INVENTION: Expression Vector Systems and  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,809B  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/209,846  
FILING DATE: March 9, 1994  
APPLICATION NUMBER: 07/789,919  
FILING DATE: No. 5925564ember 6, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 214/212  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5707 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-472-809B-8

Query Match 52.5%; Score 274.6; DB 2; Length 5707;  
Best Local Similarity 82.2%; Pred. No. 4,1e-76;

Matches 351; Conservative 0; Mismatches 24; Indels 52; Gaps 1;

1 GGACCGAGAGCGCTGCGGTGCTGAGCTGATGCTGCTCACTGCTGCTGAGAC 60  
793 GGACCGAGAGCGCTGCGGTGCTGAGCTGATGCTGCTCACTGCTGCTGAGAC 852  
61 AGGGGCTTTATTTTCAACAAGCCGACAGATAGCGCTCCAGAGTGGAGGCGACTCAG 120  
853 AGGGGCTTTATTTTCAACAAGCCGACAGATAGCGCTCCAGAGTGGAGGCGACTCAG 912  
121 ACAGGATGCTGATGATGCTGCTGCTGCGAGCTGATGCTGAGGAGGCTGAGATGATC 180  
913 ACAGGATGCTGATGATGCTGCTGCTGCGAGCTGATGCTGAGGAGGCTGAGATGATC 972  
181 TGTGCAACCCCTTAAGCCGGAAGAGCGAGCCGCTCCGCTGCGCCAGCCGACACCGAC 240  
973 TGTGCAACCCCTTAAGCCGGAAGAGCGAGCCGCTCCGCTGCGCCAGCCGACACCGAC 1032  
241 ATGCCCAAGACTCAGAGATATCAGCTCCTCATCTACCAACAAGAAATGATGCTAGAGG 300  
1033 ATGCCCAAGACTCAGAGATATCAGCTCCTCATCTACCAACAAGAAATGATGCTAGAGG 1047  
301 AGAAGAAAGAGATGATGATTTGAGAGACAGATGAGGAGGAGTGCAGAGAAACAGAACTA 360  
1048 -----AAGAGATGATGATTTGAGAGACAGATGAGGAGGAGTGCAGAGAAACAGAACTA 1100  
361 CAGGATGATGAGAGAGCCCTTGTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
1101 CAGGATGATGAGAGAGCCCTTGTGAGAGTGAAGAGATGAGATGAGAGAGAGAGAGAGAG 1160  
421 CTCTGCA 427  
1161 GGCTGCA 1167

RESULT 6  
US-08-472-809B-7  
Sequence 7, Application US/08472809B  
Patent No. 5925564

GENERAL INFORMATION:  
APPLICANT: Schwartz, Robert J.

APPLICANT: Demayo, Franco J.

TITLE OF INVENTION: Expression Vector Systems and

TITLE OF INVENTION: Method of Use

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,809B

FILING DATE: June 7, 1995

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/209,846

FILING DATE: March 9, 1994

APPLICATION NUMBER: 07/789,919

FILING DATE: No. 5925564ember 6, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 214/212

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ. ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 6345 bases

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA  
US-08-472-809B-7

Query Match 52.5%; Score 274.6; DB 2; Length 6345;  
Best Local Similarity 82.2%; Pred. No. 4,3e-76;

Matches 351; Conservative 0; Mismatches 24; Indels 52; Gaps 1;

1 GGACCGAGAGCGCTGCGGTGCTGAGCTGATGCTGCTCACTGCTGCTGAGAC 60  
3702 GGACCGAGAGCGCTGCGGTGCTGAGCTGATGCTGCTCACTGCTGCTGAGAC 3761  
61 AGGGGCTTTATTTTCAACAAGCCGACAGATAGCGCTCCAGAGTGGAGGCGACTCAG 120  
3762 AGGGGCTTTATTTTCAACAAGCCGACAGATAGCGCTCCAGAGTGGAGGCGACTCAG 3821  
121 ACAGGATGCTGATGATGCTGCTGCTGCGAGCTGATGCTGAGGAGGCTGAGATGATC 180  
3822 ACAGGATGCTGATGATGCTGCTGCTGCGAGCTGATGCTGAGGAGGCTGAGATGATC 3881  
181 TGTGCAACCCCTTAAGCCGGAAGAGCGAGCCGCTCCGCTGCGCCAGCCGACACCGAC 240  
3882 TGTGCAACCCCTTAAGCCGGAAGAGCGAGCCGCTCCGCTGCGCCAGCCGACACCGAC 3941





US-08-308-196A-1  
Sequence 1, Application US/08308196A  
Patent No. 5612198  
GENERAL INFORMATION:  
APPLICANT: Bierley, Russell A.  
APPLICANT: Davis, Geneva R.  
APPLICANT: Holtz, Gregory C.  
APPLICANT: Gleeson, Martin A.  
APPLICANT: Howard, Bradley D.  
TITLE OF INVENTION: Production of Insulin-Like Growth  
Factor-1 in Methylophilic Yeast Cells  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,196A  
FILING DATE: 09-SEPT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,523  
FILING DATE: 03-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/578,728  
FILING DATE: 04-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 51875  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)238-0999  
TELEFAX: (619)238-0062  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 14..232  
US-08-308-196A-1

Query Match 35.4%; Score 185.2; DB 1; Length 240;  
Best Local Similarity 91.6%; Pred. No. 8.6e-49;  
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GGACCGAGAGCGCTGCGGCTGCTGAGCTGATGCTCTTCAGTTCGTGTGTGAGAC 60  
DB 17 GGACCGAGAGCGCTGCGGCTGCTGAGCTGATGCTCTTCAGTTCGTGTGTGAGAC 76  
QY 61 AGGGGCTTTTATTTCACAAAGCCACAGATACGGCTCCAGAGTCGAGGGCAGCTCAG 120  
DB 77 AGGGGCTTTTATTTCACAAAGCCACAGATACGGCTCCAGAGTCGAGGGCAGCTCAG 136  
QY 121 ACAGGATGCTGATGATGCTGCTCCGAGAGTGTGATCTGAGAGGCTGAGATGTAC 180  
DB 137 ACAGGATGCTGATGATGCTGCTCCGAGAGTGTGATCTGAGAGGCTGAGATGTAT 196  
QY 181 TGTGACCCCTCAAGCCGCAAGGCAAGGCGCCGCT 214  
DB 197 TGGCACCCTCAAGCCCTGCAAGTCAAGCTTAT 230

RESULT 14  
PCT-US91-06452-1  
Sequence 1, Application PC/TUS9106452  
GENERAL INFORMATION:  
APPLICANT: Bierley, Russell A.  
APPLICANT: Davis, Geneva R.  
APPLICANT: Holtz, Gregory C.  
APPLICANT: Gleeson, Martin A.  
APPLICANT: Bradley, D. H.  
TITLE OF INVENTION: Production of Insulin-Like Growth  
Factor-1 in Methylophilic Yeast Cells  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 South LaSalle Street, Suite 900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/06452  
FILING DATE: 19910409  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/578,728  
FILING DATE: 04-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 51874  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)552-1311  
TELEFAX: (619)552-0095  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 14..232  
PCT-US91-06452-1

Query Match 35.4%; Score 185.2; DB 5; Length 240;  
Best Local Similarity 91.6%; Pred. No. 8.6e-49;  
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY 61 AGGGGCTTTTATTTCACAAAGCCACAGATACGGCTCCAGAGTCGAGGGCAGCTCAG 120  
DB 77 AGGGGCTTTTATTTCACAAAGCCACAGATACGGCTCCAGAGTCGAGGGCAGCTCAG 136  
QY 121 ACAGGATGCTGATGATGCTGCTCCGAGAGTGTGATCTGAGAGGCTGAGATGTAC 180  
DB 137 ACAGGATGCTGATGATGCTGCTCCGAGAGTGTGATCTGAGAGGCTGAGATGTAT 196  
QY 181 TGTGACCCCTCAAGCCGCAAGGCAAGGCGCCGCT 214  
DB 197 TGGCACCCTCAAGCCCTGCAAGTCAAGCTTAT 230

RESULT 15  
US-09-029-267-13

Sequence 13, Application US/09029267  
Patent No. 6107057  
GENERAL INFORMATION:  
APPLICANT: Crawford, Kenneth  
APPLICANT: Zator, Isabel  
APPLICANT: Innis, Michael  
TITLE OF INVENTION: Pichia Secretary Leader for Protein  
TITLE OF INVENTION: Expression  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: United States  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/029,267  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Chung, Ling-Fong  
REGISTRATION NUMBER: 36,482  
REFERENCE/DOCKET NUMBER: 1165.100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2704  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 390 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Synthetic"  
US-09-029-267-13

Query Match 35.4% Score 185.2; DB 3; Length 390;  
Best Local Similarity 91.6%; Pred. No. 11e-48;  
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 1 GGACCGAGAGCGCTGCGGTGCTGAGCTGTGATGCTCTTCAGTCTGTGTGAGAC 60  
DB 160 GGACCGAGAGCGCTGCGGTGCTGAGCTGTGATGCTCTTCAGTCTGTGTGAGAC 219  
QY 61 AGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCATCGAGGCGACACTCAG 120  
DB 220 AGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCATCGAGGCGACACTCAG 279  
QY 121 ACAGGCATGTGATGAGTGTCTTCGAGACTGTGATCTGAGGAGGCTGTGAGATGTAC 180  
DB 280 ACAGGCATGTGATGAGTGTCTTCGAGACTGTGATCTGAGGAGGCTGTGAGATGTAT 339  
QY 181 TGTGACACCCCTCAAGCGGCAAGGACAGCCGCT 214  
DB 340 TGTGACACCCCTCAAGCGGCTGCAAGTCAAGTGTAT 373

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Job time : 43.3965 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 17:22:19 ; Search time 94.7296 Seconds  
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7994.713 Million cell updates/sec

Title: US-09-852-261-5  
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Sequence: 1 ggaccggagacgctctgcgg.....aatacacaagtaaacatlc 523

Scoring table:  
IDENTITY-NUC  
Gapop 10.0, Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	523	100.0	523	10	US-09-852-261-5
2	467.4	89.4	517	10	US-09-852-261-1
3	409	78.2	471	10	US-09-852-261-13
4	356.8	68.2	539	10	US-09-852-261-3
5	349.4	66.8	651	9	US-10-161-088-1
6	334.4	63.9	7260	9	US-10-166-639-4
7	334.4	63.9	7260	10	US-09-819-497-24
8	334.4	63.9	7260	10	US-09-880-107-379
9	262	45.1	487	10	US-09-852-261-11
10	237.6	45.4	318	10	US-09-852-261-9
11	228	43.6	462	9	US-10-238-114-1
12	209	40.0	286	9	US-10-161-088-3
13	187	35.8	4532	10	US-09-930-377B-1
14	186.6	35.7	210	10	US-09-930-377B-2
15	185.2	35.4	390	9	US-10-179-046-13
16	141.6	27.1	213	9	US-10-076-816-9
17	141.6	27.1	213	9	US-10-077-381-9
18	127	24.3	621	9	US-10-280-826-40
19	127	24.3	621	10	US-09-921-398-40

20	113.4	21.7	480	9	US-10-280-826-38	Sequence 38, Appl
21	113.4	21.7	480	10	US-09-921-398-38	Sequence 38, Appl
22	77.2	14.8	854	9	US-09-954-531-989	Sequence 989, Appl
23	75.4	14.4	447	9	US-10-025-380-917	Sequence 917, Appl
24	75.4	14.4	447	10	US-09-922-217-917	Sequence 917, Appl
25	75.4	14.4	447	10	US-09-833-263-917	Sequence 917, Appl
26	75.2	14.4	437	9	US-10-066-543-663	Sequence 663, Appl
27	75.2	14.4	493	9	US-10-066-543-997	Sequence 997, Appl
28	75.2	14.4	536	9	US-10-066-543-1040	Sequence 1040, Appl
29	75.2	14.4	536	9	US-10-066-543-428	Sequence 428, Appl
30	75.2	14.4	539	9	US-10-136-841-1	Sequence 1, Appl
31	75.2	14.4	549	9	US-10-066-543-478	Sequence 478, Appl
32	75.2	14.4	574	9	US-10-025-380-918	Sequence 918, Appl
33	75.2	14.4	574	10	US-09-922-217-918	Sequence 918, Appl
34	75.2	14.4	574	10	US-09-833-263-918	Sequence 918, Appl
35	75.2	14.4	577	9	US-10-066-543-1137	Sequence 1137, Appl
36	75.2	14.4	579	9	US-10-066-543-1094	Sequence 1094, Appl
37	75.2	14.4	586	9	US-10-066-543-808	Sequence 808, Appl
38	75.2	14.4	1356	9	US-10-081-119-37	Sequence 37, Appl
39	75.2	14.4	1356	9	US-10-097-340-144	Sequence 144, Appl
40	75.2	14.4	1356	10	US-09-962-436-293	Sequence 293, Appl
41	75.2	14.4	1356	10	US-09-954-456-294	Sequence 294, Appl
42	75.2	14.4	1386	10	US-09-880-107-2092	Sequence 2092, Appl
43	75.2	14.4	4380	9	US-10-125-181-37	Sequence 37, Appl
44	73.8	14.1	411	10	US-09-960-352-2082	Sequence 2082, Appl
45	72	13.8	237	9	US-10-136-841-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-852-261-5  
; Sequence 5, Application US/09852261  
; Patent No. US20020083477A1  
; GENERAL INFORMATION:  
; APPLICANT: GOLDSPINK, GEOFREY  
; APPLICANT: TRENCH, GIORGIO  
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE  
; FILE REFERENCE: 117-351  
; CURRENT APPLICATION NUMBER: US/09/852,261  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: GB 0011278.9  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 523  
; TYPE: DNA  
; ORGANISM: Oryctolagus cuniculus  
US-09-852-261-5

Query Match 100.0%; Score 523; DB 10; Length 523;  
Best Local Similarity 100.0%; Pred. No. 1.2e-163;  
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	AGGGGCTTTTATTTTACACAGCCACAGATACGGCTCCAGAGTGGAGGACCTCAG	120
DB	61	AGGGGCTTTTATTTTACACAGCCACAGATACGGCTCCAGAGTGGAGGACCTCAG	120
QY	61	AGGGGCTTTTATTTTACACAGCCACAGATACGGCTCCAGAGTGGAGGACCTCAG	120
DB	61	AGGGGCTTTTATTTTACACAGCCACAGATACGGCTCCAGAGTGGAGGACCTCAG	120
QY	121	ACAGGATGTGTGATGAGTGTCTTCGAGCTGTATCTAGAGGCTGACATGTAC	180
DB	121	ACAGGATGTGTGATGAGTGTCTTCGAGCTGTATCTAGAGGCTGACATGTAC	180
QY	121	ACAGGATGTGTGATGAGTGTCTTCGAGCTGTATCTAGAGGCTGACATGTAC	180
DB	121	ACAGGATGTGTGATGAGTGTCTTCGAGCTGTATCTAGAGGCTGACATGTAC	180
QY	181	TGTGACCCCTTAAGCGGCAAGAGGAGGCTCGGCGGCGGCGGCGGCGGCGGAGC	240
DB	181	TGTGACCCCTTAAGCGGCAAGAGGAGGCTCGGCGGCGGCGGCGGCGGCGGAGC	240
QY	241	ATGCCAGAGCTCAGAGTATCAGCTCCATCTTACCAACAGAAATGAGTCTCAGAGG	300

Db	241	ATGCCCAACACCAAGATATCGCCTCATCTACCAACAGAAATGAAGTCTCAAGG	300
QY	301	AGAAGAAAGAGATACATTGTAAACAACAAGTAGAGGAGTGCAGAAACAAGACTA	360
Db	301	AGAGAGAAAGAAAGTACATTGTAAACAACAAGTAGAGGAGTGCAGAAACAAGACTA	360
QY	361	CAGAGTGTAGSAGACCCCTTCTGAGAGTGAAGAAAGACAGCCGACAGACCCCTTTS	420
Db	361	CAGAGTGTAGSAGAACCCCTTCTGAGAGTGAAGAAAGACAGCCGACAGACCCCTTTS	420
QY	421	CTCTGCACAGTTACCTGTTAAACATTCGAGATACCGGCCAAAATTAATTGATACATT	480
Db	421	CTCTGCACAGTTACCTGTTAAACATTCGAGATACCGGCCAAAATTAATTGATACATT	480
QY	481	CAAGATGCGATTTCCCCCAATGAATACAGAAATCAAGAAACATTC	523
Db	481	CAAGATGCGATTTCCCCCAATGAATACAGAAATCAAGAAACATTC	523

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1 RESULT 2
2 US-09-852-261-1
3 Sequence 1, Application US/09852261
4 Patent No. US20020083477A1
5 GENERAL INFORMATION:
6 APPLICANT: GOLDSPIRK, GEOFFREY
7 APPLICANT: TEKENSHI, GIORGIO
8 TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
9 FILE REFERENCE: 117-351
10 CURRENT APPLICATION NUMBER: US/09/852,261
11 CURRENT FILING DATE: 2001-05-10
12 PRIOR APPLICATION NUMBER: GB 0011278.9
13 PRIOR FILING DATE: 2000-05-10
14 NUMBER OF SEQ. ID NOS: 14
15 SOFTWARE: PatentIn Ver. 2.1
16 SEQ. ID NO 1
17 LENGTH: 517
18 TYPE: DNA
19 ORGANISM: Homo sapiens
20 US-09-852-261-1

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Query Match	89.4%	Score 467.4;	DB 10;	Length 517;
Best Local Similarity	96.2%;	Pred. NO. 3.7e-145;		
Matches 501; Conservative	0;	Mismatches 16;	Indels 4;	Gaps 2

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QY	61	AGGGGCTTTATTTCACACAGCCCAAGATACGGCTCCAGACGTCGAGGACCTCAG	120
Db	61	AGGGGCTTTATTTCACACAGCCCAAGATACGGCTCCAGACGTCGAGGACGCTCAG	120
QY	121	ACAGGCTATCTGGATGAGTGTCTGCTTCCGGAGCTGTGATCTGAGGAGCTGGAGATGAC	180
Db	121	ACAGGCTATCTGGATGAGTGTCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGAT	180
QY	181	TGGCACCCCTCAACCGCGCAAAGGACACCCCGCTCCGCTGGCCACGGCCACACCGAC	240
Db	181	TGGCACCCCTCAACCGCTGGCAAAGTCACTGGCTCTGCTGGCCACGGCCACACCGAC	240
QY	241	ATGCCCAAGACTCAGAAATATCAGCCTCATCTACCAACAAGAAATGAAAGTTCAGAG	300
Db	241	ATGCCCAAGACCCCAAGATATCAGCCCTCATCTACCAACAAGAAACAGAAAGTCTCA---G	297
QY	301	AGGAGGAAGGAAGTACATTTGAAAGACACAAGTAGAGGGAGTGCAGGAAACAAGACTA	360
Db	298	AGGAGGAAGGAAGTACATTTGAAAGACACAAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
QY	361	CAGGATGTGSAAGACCTTCTGAGAGGATGSAAGAAAGACACGCCACCGCAGACCTTTG	420
Db	358	CAGGATGTG--GAAGACCTTCTGAGAGTGAAGAAAGACAGGCCACCGCAGACCTTTG	416

QY	421	CTGTGCACATTTCCTGTTAAATCTGGATACCGGCGCAAAAAATTAAGTTGATCACAATT	480
	417	CTGTGCACASTTACCTGTAAATCTGGATTACCGGCGCAAAAAATTAAGTTTATCACAATT	476
QY	481	CAAGAATGGCATTTCCGCCCAATGCAATACACAAAGTAAACAT	521
Db	477	CAAGAATGGCATTTCCGCCCAATGCAATACACAAAGTAAACAT	517

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1  RESULT 3
2  US-09-852-261-13
3  : Sequence 13, Application US/09852261
4  : Patent No. US20020083477A1
5  : GENERAL INFORMATION:
6  :
7  : APPLICANT: GOLDSPINK, GEOFFREY
8  : APPLICANT: TEREHNGHI, GIORGIO
9  : TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
10 : FILE REFERENCE: 117-351
11 :
12 : CURRENT APPLICATION NUMBER: US/09/852,261
13 : CURRENT FILING DATE: 2001-05-10
14 : PRIOR APPLICATION NUMBER: GB 0011278.9
15 : PRIOR FILING DATE: 2000-05-10
16 : NUMBER OF SEQ. ID NOS: 14
17 : SOFTWARE: PatentIn Ver. 2.1
18 : SEQ ID NO 13
19 :
20 : LENGTH: 471
21 : TYPE: DNA
22 :
23 : ORGANISM: Oryzotolagus cuniculus
24 : US-09-852-261-13

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Query Match	78.2%	Score 409;	DB 10;	length 471;
Best Local Similarity	90.1%;	Pred. No. 9.6e-126;		
Matches 471;	Conservative	0;	Mismatches 0;	Indels 52; Gaps 14

QY	1	GGAGCCGAGAACCCCTCTCGCGGTCTAGCTGGTGGATGCTCTCTCAGTTCG1GTGTGGAGAC	60
Db	1	GGAGCCGAGAACCCCTCTCGCGGTCTAGCTGGTGGATGCTCTCTCAGTTCG1GTGTGGAGAC	60
QY	61	AGGGGCTTTATTTTCACAAAGCCACAGATACGGCTTCCACAGCTCGGAGGGACCTCAG	120
Db	61	AGGGGCTTTATTTTCACAAAGCCACAGATACGGCTTCCACAGCTCGGAGGGACCTCAG	120
QY	121	ACAGGCGATCGTGGATGAGTGGTGGCTTCGCGAGAGTGTATCTGAGAGAGGCTGGAGATGTAC	180
Db	121	ACAGGCGATCGTGGATGAGTGGTGGCTTCGCGAGAGTGTATCTGAGAGAGGCTGGAGATGTAC	180
QY	181	TGTGCACCCCTCAAGCCGGCAAAAGGCAGCCGCTCGTCCGTGCCCAGCCGACACCCGAC	240
Db	181	TGTGCACCCCTCAAGCCGGCAAAAGGCAGCCGCTCGTCCGTGCCCAGCCGACACCCGAC	240
QY	241	ATGCCCAAGACATCAGAGATCAGCGCTCATCTACCAACAGAAATGAAGTCTCAAGG	300
Db	241	ATGCCCAAGACATCAGAGATCAGCGCTCATCTACCAACAGAAATGAAGTCTCAAGG	300
QY	301	AGAGGAAAGAGATPACTTTGGAACACAGATAGAGGAGTGCAGAGAAACAGAACTA	360
Db	256	-----AAGGAGAGTACATTTTGAAAGAACCAAGTATAGAGGAGTGCAGAGAAACAAAGACTA	308
QY	361	CAGATGTATGGAAGACCCCTTCTGAGAGTGTGAAGAAAGGACAGCCGACGAGAGCCCTTG	420
Db	309	CAGATGTATGGAAGACCCCTTCTGAGAGTGTGAAGAAAGGACAGCCGACGAGAGCCCTTG	368
QY	421	CTCTGCACACTTACTGTAAACATGTGAATACCGGCCAAAAAATTAAGTTGATCACAATT	480
Db	369	CTCTGCACAGTATCCCTGTAAACATGTGAATACCGGCCAAAAAATTAAGTTGATCACAATT	428
QY	481	CAAGATGCGATTTTCCCCCAATGAATACCAAGATAAACATTC	523
Db	429	CAAGATGCGATTTTCCCCCAATGAATACCAAGATAAACATTC	471

RESULT 4  
DS-09-852-261-3



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; Sequence 3, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Rattus sp.
; US-09-852-261-3

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Query Match      68.2%; Score 356.8; DB 10; Length 539;
Best Local Similarity 82.3%; Pred. No. 2.4e-108;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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QY 1 GGACCGGAGAGAGCTGCGGTGCTGAGCTGCTGCTTCAAGTCTTCAAGTCTGCTGCTGAGAC 60
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Db 1 GGACCGGAGAGAGAGCTTGGGGGCTGAGCTGAGCTGAGCTTCAAGTCTTCAAGTCTGAGACA 60
QY 61 AGGCGCTTTTATTTCACAAAGCCACAGATACGGCTCCAGAGCTGGAGGCGGACCTCAG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AGGCGCTTTTACTTCAAAAGCCACAGCTATGCTCTCAGACATTCGGAGGCGGACCTCAG 120
QY 121 ACAGGCTGCTGATGATGCTGCTTCCGAGAGCTGATCTGAGAGGCTGGAGATGTAC 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ACAGGCTGCTGATGATGCTGCTTCCGAGAGCTGATCTGAGAGGCTGGAGATGTAC 180
QY 181 TGTCACCCCTCAAGCCCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 TGTCACCCCTCAAGCCCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 241 ATGCCCAAGACTCAGAGATATCAGCTTCATCTACCAACAAAGAAATGAAGTCTCAGAG 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ATGCCCAAGACTCAGAGATATCAGCTTCATCTACCAACAAAGAAATGAAGTCTCAGAG 300
QY 301 AGAAGGAAAGAGAGTACCTTGAAGAACACAGTAGAGGAGTCCAGAGAAACAGAGACTA 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 AGAAGGAAAGAGAGTACCTTGAAGAACACAGTAGAGGAGTCCAGAGAAACAGAGACTA 360
QY 361 CAGGATGTAGAGAGAGCCCTTCTGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 CAGGATGTAGAGAGAGCCCTTCTGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 CTCTGCACAGTCTTCTGTAACATTTGAAATCCGGCCA-----AAAATAGTTGATC 474
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 CTCTGCACAGTCTTCTGTAACATTTGAAATCCGGCCA-----AAAATAGTTGATC 474
QY 475 ACATTTCAAAGAT-GGCATTTCCCAATGAATACAAATGAATGAATGAATGAATGAATGA 523
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 ACATTTCAAAGAT-GGCATTTCCCAATGAATACAAATGAATGAATGAATGAATGAATGA 523
QY 481 TCATTTCAGAGATGGGCAATTTCCCTCATGAAATACCAATGAATGAATGAATGAATGA 530
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 5
US-10-161-088-1
; Sequence 1, Application US/10161088
; Publication No. US2003007761A1
; GENERAL INFORMATION:
; APPLICANT: Parrow, Vendela
; APPLICANT: Rosegren, Linda
; TITLE OF INVENTION: NEW METHODS
; FILE REFERENCE: 13425-11001
; CURRENT APPLICATION NUMBER: US/10/161,088
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: SE 0101934-8
; PRIOR FILING DATE: 2001-06-01

```

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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(471)
; US-10-161-088-1

```

```

Query Match      66.8%; Score 349.4; DB 9; Length 651;
Best Local Similarity 82.8%; Pred. No. 7.8e-106;
Matches 425; Conservative 0; Mismatches 81; Indels 7; Gaps 2;

```

```

QY 1 GGACCGGAGAGAGCTGCGGTGCTGAGCTGCTGCTTCAAGTCTTCAAGTCTGCTGCTGAGAC 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 GGACCGGAGAGAGAGCTTGGGGGCTGAGCTGAGCTGAGCTTCAAGTCTTCAAGTCTGAGACA 198
QY 61 AGGCGCTTTTATTTCACAAAGCCACAGATACGGCTCCAGAGCTGGAGGCGGACCTCAG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 199 AGGCGCTTTTACTTCAAAAGCCACAGCTATGCTTCCAGCAATTCGGAGGCGGACCTCAG 258
QY 121 ACAGGCTGCTGATGATGCTGCTTCCGAGAGCTGATCTGAGAGGCTGGAGATGTAC 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 259 ACAGGCTGCTGATGATGCTGCTTCCGAGAGCTGATCTGAGAGGCTGGAGATGTAC 318
QY 181 TGTCACCCCTCAAGCCCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 319 TGTCACCCCTCAAGCCCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 378
QY 241 ATGCCCAAGACTCAGAGATATCAGCTTCATCTACCAACAAAGAAATGAAGTCTCAGAG 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 379 ATGCCCAAGACTCAGAGATATCAGCTTCATCTACCAACAAAGAAATGAAGTCTCAGAG 438
QY 301 AGAAGGAAAGAGTACCTTGAAGAACACAGTAGAGGAGTCCAGAGAAACAGAGACTA 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 439 AGAAGGAAAGAGTACCTTGAAGAACACAGTAGAGGAGTCCAGAGAAACAGAGACTA 498
QY 361 CAGGATGTAGAGAGAGCCCTTCTGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 499 CAGGATGTAGAGAGAGCCCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558
QY 421 CTCTGCACAGTTCCTGTAACATTTGAAATCCGGCCA-----AAAATAGTTGATC 474
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 559 CTCTGTGAGCAACCTGCAAAACATTCGAACACCTTACCAATGAATGAATGAATGAATGA 618
QY 475 ACATTTCAAAGAT-GGCATTTCCCAATGAATACAAATGAATGAATGAATGAATGAATGA 506
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 619 ACATTTCAAAGATGGGCAATTTCCCTCATGAAATACCAATGAATGAATGAATGAATGA 651

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RESULT 6
US-10-136-639-4
; Sequence 4, Application US/10136639
; Publication No. US20030072761A1
; GENERAL INFORMATION:
; APPLICANT: Lebowitz, Jonathan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS THE BLO
; FILE REFERENCE: SYM-008
; CURRENT APPLICATION NUMBER: US/10/136,639
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 60/329,650
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 4
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-136-639-4

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Db 491 TGGGACACCCCTCAAGCCCTGCAAGCTCAGCTCTGCTCCGTCGCCACGCCACACCCGAC 550  
QY 241 ATGCCCAAGACTCAGAAATATCAGACCTCCATCTACCAACAAGAAATGAAGTCTCAGAGG 300  
Db 551 ATGCCCAAGACCCAG----- 565  
QY 301 AGAAGAAAGAAAGTACATTTGAAGAACACAGATAGAGGGAGGACAGAAACAAGAACTA 360  
Db 566 -----AAGAAAGTACATTTGAAGAAAGCAAGTAGAGGGAGGACAGAAACAAGAACTA 618  
QY 361 CAGGATGTAGAAAGACCCCTTCTGAGAGTGAAGAGACAGCCACCGCAGACCCCTTTG 420  
Db 619 CAGATGTAGAAAGACCCCTCTGAGAGTGAAGAGTACATGCCACCGCAGATCTTTG 678  
QY 421 CTCTGCAC-AGTTACTCTG-TAAACATTTGATACCCGCAAAAATAGTTGATACAT 478  
Db 679 CTCTGCACAGAGTTACCTGTTAACTTTGGAACACCTCCAAAAATAGTTGATACAT 738  
QY 479 TTCAAAGAT-GGCATTTTCCCAATGAATACACAACTAAACATTC 523  
Db 739 TTAAGAATGGGCGTTTCCCAATGAATACACAACTAAACATTC 784

## RESULT 9

US-09-852-261-11  
Sequence 11, Application US/09852261  
Patent No. US20020083477A1  
GENERAL INFORMATION:  
APPLICANT: GOLDSPIK, GEOFFREY  
APPLICANT: TEREHGT, GIORGIO  
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE  
FILE REFERENCE: 117-351  
CURRENT APPLICATION NUMBER: US/09/852,261  
CURRENT FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: GB 0011278.9  
PRIOR FILING DATE: 2000-05-10  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 11  
LENGTH: 487  
TYPE: DNA  
ORGANISM: Rattus sp.  
US-09-852-261-11

Query Match 50.1%; Score 262; DB 10; Length 487;  
Best Local Similarity 74.7%; Pred. No. 8.1e-77;  
Matches 396; Conservative 0; Mismatches 75; Indels 59; Gaps 3;

QY 1 GGAACCGAGAGCGCTGCGGCTGCTGAGCTGATGCTCTTCAATTCGTTGTTGAGAC 60  
Db 1 GGAACCAAGACCGCTTGGCGGGCTGAGCTGATGCTCTTCAATTCGTTGTTGAGAC 60  
QY 61 AGGGGCTTTATTTCAACAAGCCCAAGATAGCGCTCCAGCAGTGGAGGGACCTCAG 120  
Db 61 AGGGGCTTTATTTCAACAAGCCCAAGATAGCGCTCCAGCAGTGGAGGGACCTCAG 120  
QY 61 AGGGGCTTTATTTCAACAAGCCCAAGATAGCGCTCCAGCAGTGGAGGGACCTCAG 120  
Db 61 AGGGGCTTTATTTCAACAAGCCCAAGATAGCGCTCCAGCAGTGGAGGGACCTCAG 120  
QY 121 ACAGCATCGTGTGATGATGCTGCTCCGAGCTGATGCTGAGGAGGCTGAGATGTAC 180  
Db 121 ACAGCATCGTGTGATGATGCTGCTCCGAGCTGATGCTGAGGAGGCTGAGATGTAC 180  
QY 121 ACAGCATCGTGTGATGATGCTGCTCCGAGCTGATGCTGAGGAGGCTGAGATGTAC 180  
Db 121 ACAGCATCGTGTGATGATGCTGCTCCGAGCTGATGCTGAGGAGGCTGAGATGTAC 180  
QY 181 TGTGCAACCCCTCAAGCGGCAAGGACGCGCTCCGCTCCGTCAGGCGCAACACCGAC 240  
Db 181 TGTGCAACCCCTCAAGCGGCAAGGACGCGCTCCGCTCCGTCAGGCGCAACACCGAC 240  
QY 181 TGTGCAACCCCTCAAGCGGCAAGGACGCGCTCCGCTCCGTCAGGCGCAACACCGAC 240  
Db 181 TGTGCAACCCCTCAAGCGGCAAGGACGCGCTCCGCTCCGTCAGGCGCAACACCGAC 240  
QY 241 ATGCCCAAGACTAGAAATATCAGCTCCTACCAACAAGAAATGAAGTCTCAGAGG 300  
Db 241 ATGCCCAAGACTAG----- 255  
QY 301 AGAAGAAAGAAAGTACATTTGAAGAACACAGTAGAGGAGTGAAGAAACAAGAACTA 360  
Db 256 -----AAGAAAGTACACTTTGAAGAAACAAGTAGAGGAAAGTGAAGAAACAAGAACTA 308

QY 361 CAGATGTAGAAAGACCCCTTCTGAGATGTAAGAGACAGGCCACCGCAGACCCCTTTG 420  
Db 309 CAGAAATGTAGAGAGAGACCTCCCGAGAGACAGAAATGCGCACCGCAAGATCCTTTG 368  
QY 421 CTCTGCACAGTTACCTGTAAACATTTGATACCGGCA-----AAAATAGTTGATC 474  
Db 369 CTCTGTGACACACCTCCAAACATGGAACACCTGCGCAAAATATCTAATATGATTCATA 428  
QY 475 ACATTTCAAGAT-GGCATTTTCCCAATGAATACACAACTAAACATTC 523  
Db 429 TCAATTCAGAGATGGGCGATTTCCCTCAATGAATATACAACTAAACATTC 478

## RESULT 10

US-09-852-261-9  
Sequence 9, Application US/09852261  
Patent No. US20020083477A1  
GENERAL INFORMATION:  
APPLICANT: GOLDSPIK, GEOFFREY  
APPLICANT: TEREHGT, GIORGIO  
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE  
FILE REFERENCE: 117-351  
CURRENT APPLICATION NUMBER: US/09/852,261  
CURRENT FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: GB 0011278.9  
PRIOR FILING DATE: 2000-05-10  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 9  
LENGTH: 318  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-852-261-9

Query Match 45.4%; Score 237.6; DB 10; Length 318;  
Best Local Similarity 94.6%; Pred. No. 8.5e-69;  
Matches 246; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGAACCGAGAGCGCTGCGGCTGCTGAGCTGATGCTCTTCAATTCGTTGTTGAGAC 60  
Db 1 GGAACCGAGAGCGCTGCGGCTGCTGAGCTGATGCTCTTCAATTCGTTGTTGAGAC 60  
QY 61 AGGGGCTTTATTTCAACAAGCCCAAGATAGCGCTCCAGCAGTGGAGGGACCTCAG 120  
Db 61 AGGGGCTTTATTTCAACAAGCCCAAGATAGCGCTCCAGCAGTGGAGGGACCTCAG 120  
QY 121 ACAGCATCGTGTGATGATGCTGCTCCGAGCTGATGCTGAGGAGGCTGAGATGTAC 180  
Db 121 ACAGCATCGTGTGATGATGCTGCTCCGAGCTGATGCTGAGGAGGCTGAGATGTAC 180  
QY 181 TGTGCAACCCCTCAAGCGGCAAGGACGCGCTCCGCTCCGTCAGGCGCAACACCGAC 240  
Db 181 TGTGCAACCCCTCAAGCGGCAAGGACGCGCTCCGCTCCGTCAGGCGCAACACCGAC 240  
QY 241 ATGCCCAAGACTAGAAATATCAGCTCCTACCAACAAGAAATGAAGTCTCAGAGG 300  
Db 241 ATGCCCAAGACTAGAAATATCAGCTCCTACCAACAAGAAATGAAGTCTCAGAGG 300

## RESULT 11

US-10-238-114-1  
Sequence 1, Application US/10238114  
Patent No. US20030100073A1  
GENERAL INFORMATION:  
APPLICANT: Meritai  
APPLICANT: ANDREONI, Christine Michele  
TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST FELINE  
FILE REFERENCE: 454313-3165.1  
CURRENT APPLICATION NUMBER: US/10/238,114  
CURRENT FILING DATE: 2002-09-10  
PRIOR APPLICATION NUMBER: FR 01 11736  
PRIOR FILING DATE: 2001-09-11  
PRIOR APPLICATION NUMBER: US 60/318,666



TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: IGF-I  
US-09-930-377B-2

Query Match  
Best Local Similarity 35.7%; Score 186.6; DB 10; Length 210;  
93.3%; Pred. No. 6.4e-52;  
Matches 195; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGCGCTGCGGCTGCTGAGCTGCTGATGCTCTTCAGTCTGCTGCTGCTGAGAC 60  
DB 1 GGACCGGAGAGCGCTGCTGCGGCTGCTGAGCTGCTGATGCTCTTCAGTCTGCTGCTGAGAC 60  
61 AGGGGCTTTTATTTCACAAAGCCCAAGATACGAGCTCCAGCAGTCCGAGGCGCACTCTCAG 120  
QY 61 AGGGGCTTTTATTTCACAAAGCCCAAGATACGAGCTCCAGCAGTCCGAGGCGCACTCTCAG 120  
DB 61 AGGGGCTTTTATTTCACAAAGCCCAAGATACGAGCTCCAGCAGTCCGAGGCGCACTCTCAG 120  
QY 121 ACAGGCATCGTGATGATGATGCTGCTCCGAGCTGTGATCTGAGAGAGGCTGAGATGTAC 180  
DB 121 ACAGGCATCGTGATGATGATGCTGCTCCGAGCTGTGATCTGAGAGAGGCTGAGATGTAT 180  
QY 181 TGTGCACCCCTCAAGCGCGCAAGGCAAGC 209  
DB 181 TGTGCACCCCTCAAGCGCGCAAGGCAAGC 209  
181 TGGCGACCCCTCAAGCGCTGCCAAGTCAAGC 209

RESULT 15  
US-10-179-046-13  
Sequence 13, Application US/10179046  
Publication No. US20030013154A1  
GENERAL INFORMATION:  
APPLICANT: Crawford, Kenneth  
Zator, Isadel  
Innis, Michael  
TITLE OF INVENTION: Pichia Secretary Leader for Protein  
Expression  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESS: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: United States  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/179,046  
FILING DATE: 25-Jun-2002  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/029,267  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chung, Ling-Fong  
REGISTRATION NUMBER: 36,482  
REFERENCE/DOCKET NUMBER: 1165,100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2704  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 390 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Synthetic"  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-10-179-046-13

Query Match  
Best Local Similarity 35.4%; Score 185.2; DB 9; Length 390;  
91.6%; Pred. No. 2.0e-51;  
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGCGCTGCGGCTGCTGAGCTGCTGATGCTCTTCAGTCTGCTGCTGAGAC 60  
DB 160 GGACCGGAGAGCGCTGCGGCTGCTGAGCTGCTGATGCTCTTCAGTCTGCTGCTGAGAC 219  
QY 61 AGGGGCTTTTATTTCACAAAGCCCAAGATACGAGCTCCAGCAGTCCGAGGCGCACTCTCAG 120  
DB 220 AGGGGCTTTTATTTCACAAAGCCCAAGATACGAGCTCCAGCAGTCCGAGGCGCACTCTCAG 279  
QY 121 ACAGGCATCGTGATGATGATGCTGCTCCGAGCTGTGATCTGAGAGAGGCTGAGATGTAC 180  
DB 280 ACAGGCATCGTGATGATGATGCTGCTCCGAGCTGTGATCTGAGAGAGGCTGAGATGTAT 339  
QY 181 TGTGCACCCCTCAAGCGCGCAAGGCAAGC 214  
DB 340 TGGCGACCCCTCAAGCGCTGCCAAGTCAAGT 373

Search completed: June 15, 2003, 20:22:26  
Job time : 95.7296 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:41:03 ; Search time 1112.58 Seconds

(without alignments)  
7613.181 Million cell updates/sec

Title: US-09-852-261-5

Perfect score: 523

Sequence: 1 ggaacggagagcgtctgcg9.....aaatacaagaagtaaacattc 523

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: em\_estda:\*  
2: em\_esthda:\*  
3: em\_estln:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hnc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hnc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_jov:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vtl:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	364.8	69.8	558	9	AI503976 vm43d08.x
C 2	363	69.4	623	10	AM146128 um37e10.x
C 3	348.2	66.6	549	9	AI169253 EST215088
C 4	347	66.3	558	9	AI1265629 u104b07.x
C 5	339.2	64.9	816	9	AI119218 ue94h02.x
C 6	334.8	64.0	594	12	BF383724 602044632

C 7	322.2	61.6	499	10	AM495481
C 8	320.8	61.3	642	9	AI876493
C 9	320.8	61.3	673	14	BM984670
C 10	316.8	60.6	575	9	AI248089
C 11	309.2	59.1	468	9	AI169770
C 12	305	58.3	498	9	AA542914
C 13	299	57.2	882	9	AI604642
C 14	296.4	56.7	653	14	BQ200567
C 15	291.6	55.8	527	9	AA913900
C 16	271.6	51.9	521	10	AM493459
C 17	271.6	51.9	559	13	BI715603
C 18	271.6	51.9	621	13	BI221656
C 19	270.6	51.7	595	9	AI573421
C 20	270	51.6	499	13	BI676839
C 21	266.8	51.0	500	9	AA945553
C 22	266.8	51.0	525	9	AA963258
C 23	266	50.9	665	9	AA690767
C 24	265.2	50.7	559	13	BI715465
C 25	263.8	50.4	799	9	AI314558
C 26	263.6	50.4	525	9	AI599751
C 27	261.4	50.0	499	13	BI294072
C 28	260.4	49.8	561	13	BI714874
C 29	258.4	49.4	502	9	AI104669
C 30	258	49.3	564	13	BI714981
C 31	254.8	48.7	430	9	AI478804
C 32	254.8	48.7	558	13	BI715475
C 33	250.8	48.0	512	9	AI876203
C 34	248.2	47.5	637	10	AM413016
C 35	246.4	47.1	473	9	AA451360
C 36	246.4	47.1	486	9	AA933659
C 37	246.2	47.1	773	13	BI144500
C 38	243.2	46.5	482	9	AA456717
C 39	243	46.5	474	9	AI526955
C 40	240.8	46.0	465	9	AA277619
C 41	237.6	45.4	470	9	AI333293
C 42	237.6	45.4	608	9	AI599807
C 43	235.8	45.1	567	9	AI326648
C 44	233.2	44.6	356	10	AM297586
C 45	232.8	44.5	538	9	AA245300

## ALIGNMENTS

RESULT 1  
AI503976/c 558 bp mRNA linear EST 11-MAR-1999  
DEFINITION  
vm43d08.x1 Stratagene mouse diaphragm (9937303) Mus musculus cDNA  
Clone IMAGE:1001007 3', similar to gb:X04482 Mouse mRNA for  
preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION  
AI503976  
VERSION  
AI503976.1 GI:4401827

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
house mouse.  
Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 558)  
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person  
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter  
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
Waterston,R. and Wilson,R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Maria M/Mashu-NCI Mouse EST Project 1999  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:565223  
This clone was previously sequenced on the 5' end only, this new data is from the 3' end  
High quality sequence stop: 440.  
Location/Qualifiers  
1. .558  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1001007"  
/clone\_lib="Stratagene mouse diaphragm (#937303)"  
/tissue\_type="diaphragm"  
/dev\_stage="adult"  
/lab\_host="SOLR (Xananycin resistant)"  
/note="Organ: diaphragm; Vector: pBluescript SK-; Site: 1; EcoRI; Site: 2: XhoI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oligo dt. Average insert size: 1.5 kb. Uni-ZAP XR vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'."

BASE COUNT 103 a 133 c 149 g 173 t  
ORIGIN

Query Match 69.8%; Score 364.8; DB 9; Length 558;  
Best Local Similarity 83.2%; Pred. No. 48-90; Indels 7; Gaps 2;  
Matches 441; Conservative 0; Mismatches 82; Indels 7; Gaps 2;

1 GCACCGGAGACGCTCTGCGGTGCTGAGCTGTGATGCTCTTCAGTCTGTGTGAGAC 60  
|||||  
530 GCACGAGAGACCCCTTTGGGGGCTGAGCTGTGATGCTCTTCAGTCTGTGTGAGAC 471  
61 AGGGGCTTTATTTTGAACAAGCCACAGGATACGGCTCCAGCAGTCGAGGCGACCTAG 120  
|||||  
470 AGGGGCTTTATTTTGAACAAGCCACAGGATACGGCTCCAGCAGTCGAGGCGACCTAG 411  
121 ACAGGATGCTGATGATGATGCTCTTCGAGAGCTGTGATGAGAGAGCTGAGATGAC 180  
|||||  
410 ACAGGATGCTGATGATGATGCTCTTCGAGAGCTGTGATGAGAGAGCTGAGATGAC 351  
181 TGTGCAACCCCTTAACCCGGAAGAGCAGCCGCTCCGCTGCCAGCGCCACACGAC 240  
|||||  
350 TGTGCAACCCCTTAACCCGGAAGAGCAGCCGCTCCGCTGCCAGCGCCACACGAC 291  
241 ATGCCAGAGCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
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290 ATGCCAGAGCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 231  
301 AGAAGGAAGAGAGTACATTTGAGAGACACAAGTAGAGAGAGTGCAGAGAAACAAGACTA 360  
|||||  
230 AGAAGGAAGAGAGTACATTTGAGAGACACAAGTAGAGAGAGTGCAGAGAAACAAGACTA 171  
361 CAGATGTAGAGAGAGCTCTCCAGGAGACAGAAATGCGACATACCGGAGATCCTTG 420  
|||||  
170 CAGATGTAGAGAGAGCTCTCCAGGAGACAGAAATGCGACATACCGGAGATCCTTG 111  
421 CTCTCACAAGTTACTGTAAACATTTGATACCGGCA-----AAAAATAAGTTGATC 474  
|||||  
110 CTGCTTGAAGACCTGCAAAACATGAAACACTACCAATACAAATTAATGTCATA 51  
475 ACATTTCAAGAT-GGCAATTTCCCAATGAAATACCAATGAAATGAAATGAAATG 523  
50 ACATTTCAAGATGCGCATTTTCCCAATGAAATGAAATGAAATGAAATGAAATG 1

RESULT 2  
AW146128 623 bp mRNA linear EST 10-OCT-2000  
LOCUS AW146128/c  
DEFINITION um37el0.x1 sugano mouse embryo mewa Mus musculus cDNA clone  
IMAGE:2247498 3' similar to gp:X04462 Mouse mRNA for  
Pleiotrophin-like growth factor IB (MOUSE); mRNA sequence.  
ACCESSION AW146128  
VERSION AW146128.1 GI:6167864  
KEYWORDS EST.  
SOURCE house mouse.

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 623)  
Marras, M., Hallier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person,  
R., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Rittler,  
W., Kohn, S., Shin, T., Jackson, T., Cardenas, M., McCann, R.,  
Waterson, R. and Wilson, R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)

## AUTHORS

TITLE  
JOURNAL  
COMMENT  
Contact: Marra M/Mashu-NCI Mouse EST Project 1999  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MG1:1006958

Seq primer: custom primer used  
High quality sequence stop: 499.  
Location/Qualifiers  
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/organism="Mus musculus"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="IMAGE:2247498"  
/clone\_lib="Sugano mouse embryo mewa"  
/dev\_stage="embryo, 14 dpc"  
/lab\_host="DH10B"  
/note="Vector: pME18S-FL3; site: 1: DraIII (CACTGATG);  
site: 2: DraIII (CAGCATGTG); 1st strand cDNA was primed  
with an oligo(dT) primer [ATGAGGCTTTTCTTTTCTTTT];  
double-stranded cDNA was ligated to a DraIII adaptor  
[TTTGGCTCTACTGG], digested and cloned into distinct DraIII  
sites of the pME18S-FL3 vector (5' site CAGCATGTG, 3' site  
CACTGATG). XhoI should be used to isolate the cDNA  
insert. Size selection was performed to exclude fragments  
<1.5kb. Library constructed by Dr. Sumio Sugano  
(University of Tokyo Institute of Medical Science).  
Custom primers for sequencing: 5' end primer  
CTCTGCTCAAAAGCTCGC and 3' end primer  
CGACCTGCAAGCTCGAGCA."

## FEATURES

Source

BASE COUNT 123 a 138 c 170 g 191 t 1 others  
ORIGIN

Query Match 69.4%; Score 363; DB 10; Length 623;  
Best Local Similarity 81.9%; Pred. No. 1.3e-89;  
Matches 433; Conservative 0; Mismatches 90; Indels 6; Gaps 1;

1 GCACCGGAGACGCTCTGCGGTGCTGAGCTGTGATGCTCTTCAGTCTGTGTGAGAC 60  
|||||  
541 GCACGAGAGACCCCTTTTCGGGCTGAGCTGTGATGCTCTTCAGTCTGTGTGAGAC 482  
61 AGGGGCTTTATTTTGAACAAGCCACAGATAGAGCTCCAGCAGTGTGAGAGCAGCTAG 120  
|||||  
481 AGGGGCTTTATTTTGAACAAGCCACAGATAGAGCTCCAGCAGTGTGAGAGCAGCTAG 422  
121 ACAGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
|||||  
421 ACAGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 362  
181 TGTGCAACCCCTTAACCCGGAAGAGCAGCCGCTCCGCTGCCAGCGCCACACGAC 240  
|||||  
361 TGTGCAACCCCTTAACCCGGAAGAGCAGCCGCTCCGCTGCCAGCGCCACACGAC 302  
241 ATGCCAGAGCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
|||||  
301 ATGCCAGAGCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 242  
301 AGAAGGAAGAGAGTACATTTGAGAGACACAAGTAGAGAGTGCAGAGAAACAAGACTA 360  
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Db      241 AGAAGGAAAGAGTACATTGAGAACCCCAAGTAGAGGAGTCCAGGAACAAGACCTA 182
QY      361 CAGATGTAGAGAGACCCCTTGTGAGAGTGAAGAGACAGCCGACAGACCTTTG 420
Db      181 CAGATGTAGAGAGAGCCCTCCAGGAGACAGAAATGATGCATCACCAGGAGATCCTTG 122
QY      421 CTCGACAGAGTACCTGTAACATTTGGAATCCGCCA-----AAATATGATTATC 474
Db      121 CTGCTTGAGCAACCTGCAAAACATCGAAACCCCTTAACAAATACAAATATAGTCCATA 62
QY      475 ACATTTCAAGATGAGCATTTTCCCAATGAATACAGATTAACATTC 523
Db      61 ACATTAACAAGATGGCATTTCCCAATGAATATACAGATTAACATTC 13

RESULT 3
LOCUS   A1169253 549 bp mRNA linear EST 08-JAN-1999
DEFINITION ESTJ15088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
ACCESSION A1169253
VERSION   A1169253
KEYWORDS EST. GI:4134375
SOURCE   Rattus sp.
ORGANISM Rattus sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 549)
AUTHORS Lee,N.H., Glodok,A., Chandra,I., Mason,T.M., Quackenbush,J.,
          Kerlavage,A.R. and Adams,M.D.
          Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat
          Unpublished (1998)
          On Oct 6, 1998 this sequence version replaced gi:3705561.
          Other ESTs: TC50779
          Contact: Lee, N.H.
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21
FEATURES
         Source
         Location/Qualifiers
             1..349
             /organism="Rattus sp."
             /db_xref="taxon:10118"
             /clone="RK1BP33"
             /clone_lib="Normalized rat kidney, Bento Soares"
             /note="Organ: kidney; Vector: pT73Pac; Site_1: EcoRI;
             Site_2: NotI"
BASE COUNT 112 a 140 c 133 g 164 t
ORIGIN
Query Match 56.6%; Score 348.2; DB 9; Length 549;
Best Local Similarity 81.8%; Pred. No. 1.5e-85;
Matches 428; Conservative 0; Mismatches 88; Indels 7; Gaps 2;
QY      8 AGAGCGCTGCGGTGAGCTGTGAGTCTTTCAGTTCGTGTGAGACAGGGCT 67
Db      549 AGAGCGCTTTCGCGGGGTGAGCTGTGAGCTTTCAGTTCGTGTGAGACAGGGCT 490
QY      68 TTTATTTCAACAGCCCAAGATAGGCTCCAGCAGTGGAGAGCACTCCAGACAGGA 127
Db      489 TTTACTTCAACAGCCCAAGATAGGCTCCAGCAGTGGAGAGCACTCCAGACAGGA 430
QY      128 TCGTGAATGAGTCTCTCCGAGCTGTGATCTGAGAGCGTGAATGTACTGTGAC 187
Db      429 TTTGATGATGAGTCTCTCCGAGCTGTGATCTGAGAGCGTGAATGTACTGTGAC 370
QY      188 CCTCAAGCGGGAAGGAGAGCCCGCTCCGCTCGGTGCCAGGCGCCAGACAGATGCCA 247
Db      369 CGCTGAAGCGCTCAAGAGTACGCTTCATCCGCGGCCAGGCCACATTTGACATGCCA 310

```

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QY      248 AGACTGAGAGTATCAGCCCTCATCTACCAACAGAGAAATGANGTCTCAGAGAGAGA 307
Db      309 AGACTGAGAGTCCCAAGCCCTTTCGACACAGAGAAAGAGATGCGCAAGAGAGA 250
QY      308 AAGGATACATTTTGAAGAACACAGAGTAGAGAGTGCAGAGAAACAGACTACAGATG 367
Db      249 AAGGAGTACACTTGAAGAACACAGAGTAGAGAGTGCAGAGAAACAGACTACAGATG 190
QY      368 TAGGAGAGCCCTCTGAGAGGTGAAGAGAGAGAGAGAGAGCCAGGACCTTGTCTGCA 427
Db      189 TAGGAGAGCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 130
QY      428 CAGTTACCTGTAACATTTGAGATACCGGCCA-----AAATATGATTGATCATTC 481
Db      129 AGCAACCTGCAAAACATCGGAACACCTCGCAATATCATATGATTTAATACCATTC 70
QY      482 AAGAT-GGCATTTTCCCAATGAATACAGATTAACATTC 523
Db      69 AGAGATGGCATTTTCCCTCAATGAATACAGATTAACATTC 27

RESULT 4
LOCUS   A1265629 558 bp mRNA linear EST 18-NOV-1998
DEFINITION U044807.x1 Sugano mouse liver mla Mus musculus cDNA clone
          IMAGE:1890901 3' similar to gb:X04482 Mouse mRNA for
          preproinsulin-like growth factor IB (MOUSE)., mRNA sequence.
ACCESSION A1265629
VERSION   A1265629
KEYWORDS EST. GI:3883787
SOURCE   Mus mouse.
ORGANISM Mus musculus.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          1 (bases 1 to 558)
REFERENCE 1
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
          Geisel,S., Kucaba,T., Lacy,M., Le,M., Matlin,J., Morris,M.,
          Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
          Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
          Waterston,R.
          The WashU-HMIT Mouse EST Project
          Unpublished (1996)
          Contact: Maria M/Mouse EST Project
          WashU-HMIT Mouse EST Project
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: mouseest@watson.wustl.edu
          This clone is available royalty-free through LINTL; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          MGI:975225
          Seq primer: custom primer used
          High quality sequence stop: 495.
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             /strain="C57BL"
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             /sex="female"
             /dev_stage="adult"
             /lab_host="DH10B"
             /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
             (CACTGATG); Site_2: DraIII (CAACCATGTC); 1st strand cDNA
             was primed with an o1190(drf) primer
             [ATGAGGCGCTTTTATTTTATTTT]; double-stranded cDNA was
             ligated to a DraIII adaptor [TGTGGCGCTTACTG]; digested
             and cloned into distinct DraIII sites of the pME18S-FL3
             vector (5' site CACTGATG, 3' site CAACCATG); XhoI
             be used to isolate the cDNA insert. Size selection was

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performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTCTAAAGCTGG and 3' end primer CGACCTGACGCTCGACACA."

BASE COUNT 106 a 135 c 156 g 161 t

Query Match 66.3%; Score 347; DB 9; Length 558;  
Best Local Similarity 82.0%; Pred. No. 3.3e-85;  
Matches 414; Conservative 0; Mismatches 85; Indels 6; Gaps 1;

1 GGACCGAGAGCGCTGCGGTGCTGAGCTGTGATGCTCTTCAGTCTGTGTGAGAC 60  
506 GGACCGAGAGCGCTGCGGTGCTGAGCTGTGATGCTCTTCAGTCTGTGTGAGAC 447  
61 AGGGGCTTTTATTTTCAACAAGCCACAGATAGGCTCCAGAGTGGAGGCGACCTGAG 120  
446 AGGGGCTTTTATTTTCAACAAGCCACAGATAGGCTCCAGAGTGGAGGCGACCTGAG 387  
121 ACAGGATGCTGATGATGCTGCTGCGAGCTGTGATGATGAGGAGCTGGAGATGATAC 180  
386 ACAGGATGCTGATGATGCTGCTGCGAGCTGTGATGATGAGGAGCTGGAGATGATAC 327  
181 TGTGCAACCCCTCAAGCCGCAAGAGCAGCCGCTCCGCTGCGCCAGCGCCACACGAC 240  
326 TGTGCCCCACTGAGGCTCAACAAAGCAGCCGCTCTATCCGTCAGGCGCCACACTGAC 267  
241 ATGCCAAGACTGAGAGTATGAGCTGCTGATGATGATGATGATGATGATGATGATGAT 300  
266 ATGCCAAGACTGAGAGTATGAGCTGCTGATGATGATGATGATGATGATGATGATGAT 207  
301 AGAAGAAAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
206 AGAAGAAAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 147  
361 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
146 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 87  
421 CTCTGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474  
86 CTCTGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 27  
475 ACATTTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 499  
26 ACATTTCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2

RESULT 5  
A119218 816 bp mRNA linear EST 02-SEP-1998  
LOCUS u94h02.y1 Sugano mouse embryo mewa Mus musculus cDNA clone  
DEFINITION IMAGE:149803.5, similar to gb:U0482 Mouse mRNA for  
preproinsulin-1-like growth factor IB (MOUSE);, mRNA sequence.  
A119218.1 GI:3519542  
EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 816)  
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Duparque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,  
Theising, R., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Maria M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:936407  
Seq primer: custom primer used  
High quality sequence stop: 473.  
Location/Qualifiers  
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/organism="Mus musculus"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="IMAGE:149803"  
/dev\_stage="embryo, 14 dpc"  
/lab\_host="DH10B"  
/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGCTG);  
Site 2: DraIII (CACCATG); 1st strand cDNA was primed  
with an oligo(dT) primer (ATGGGCTTTTATTTTATTTT);  
double-stranded cDNA was ligated to a DraIII adaptor  
(TGTGGCTGCTGCTG), digested and cloned into distinct DraIII  
sites of the pME18S-FL3 vector (5' site CACTGCTG, 3' site  
CACCATG). XhoI should be used to isolate the cDNA  
insert. Size selection was performed to exclude fragments  
<1.5kb. Library constructed by Dr. Sumio Sugano  
(University of Tokyo Institute of Medical Science).  
Custom primers for sequencing: 5' end primer  
CTCTGCTCTAAAGCTGG and 3' end primer  
CGACCTGACGCTCGACACA."

BASE COUNT 230 a 219 c 172 g 187 t 8 others

Query Match 64.9%; Score 339.2; DB 9; Length 816;  
Best Local Similarity 81.2%; Pred. No. 5.4e-83;  
Matches 389; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

1 GGACCGAGAGCGCTGCGGTGCTGAGCTGTGATGCTCTTCAGTCTGTGTGAGAC 60  
323 GGACCGAGAGCGCTGCGGTGCTGAGCTGTGATGCTCTTCAGTCTGTGTGAGAC 382  
61 AGGGGCTTTTATTTTCAACAAGCCACAGATAGGCTCCAGAGTGGAGGCGACCTGAG 120  
383 AGGGGCTTTTATTTTCAACAAGCCACAGATAGGCTCCAGAGTGGAGGCGACCTGAG 442  
121 ACAGGATGCTGATGATGCTGCTGCGAGCTGTGATGATGATGATGATGATGATGATGAT 180  
443 ACAGGATGCTGATGATGCTGCTGCGAGCTGTGATGATGATGATGATGATGATGATGAT 502  
181 TGTGACCCCTCAAGCCGCAAGAGCAGCCGCTCCGTCGCCAGCGCCACACCGAC 240  
503 TGTGACCCCTCAAGCCCTTACAAAAGCAGCCGCTCTATCCGTCGCCAGCGCCACAC 562  
241 ATGCCAAGACTGAGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 300  
563 ATGCCAAGACTGAGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 622  
301 AGAAGAAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
623 AGAAGAAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 682  
361 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
683 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 742  
421 CTCTGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479  
743 CTCTGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 801

RESULT 6  
BF383724

LOCUS BF383724 594 bp mRNA linear EST 27-NOV-2000  
 DEFINITION 602044632F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:4194295 5',  
 mRNA sequence.  
 ACCESSION BF383724  
 VERSION BF383724.1 GI:11365029  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 594)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: rgs@phs-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L1M9527 row: p column: 08  
 High quality sequence stop: 389.  
 Location/Qualifiers  
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 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4194295"  
 /clone\_lib="NCI\_CGAP\_L19"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: liver; Vector: pCMV-Sport6; Site: 1; NotI;  
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.9 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."  
 BASE COUNT 175 a 162 c 142 g 115 t  
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 Query Match 64.0%; Score 334.8; DB 12; Length 594;  
 Best Local Similarity 82.0%; Pred. No. 8.1e-82;  
 Matches 400; Conservative 0; Mismatches 82; Indels 6; Gaps 1;  
 16 TGGGTTGCTGAGCTGGTGGATGCTCTTCAGTCTGTGTGGAGACAGGGCTTTATTTC 75  
 107 TGGGGGCTGAGCTGGTGGATGCTCTTCAGTCTGTGTGGAGACAGGGCTTTATTTC 166  
 76 AACAAAGCCACAGATAGCGCTCCAGACAGTGGAGGGGACCTCAGACAGGATGAT 135  
 167 AACAAAGCCACAGCTATGCTCCAGACAGTGGAGGGGACCTCAGACAGGATGAT 226  
 136 GAGTGTCTCTCCGAGCTGTGATCTGAGAGGCTGGAGATGTACTGTGACCCCTCAG 195  
 227 GAGTGTCTCTCCGAGCTGTGATCTGAGAGGCTGGAGATGTACTGTGACCCCTCAG 286  
 196 CCGGAAGAGGAGCCGCTCCGTCGCGCCAGGCGCAACCGACATGCCCAACACACAG 255  
 287 CCTACAAAGAGAGCCGCTCTATCCGTCGCGCCAGGCGCAACCTGACATGCCCAACAC 346  
 256 AAGTATCAGCCTCATCTACCAACAGAAAATGAAGTCTGAGAGAGAGAAAGAGT 315  
 347 AAGTATCAGCCTCATCTACCAACAGAAAATGAAGTCTGAGAGAGAGAAAGAGT 406  
 316 ACATTGGAAGAACAGTAGAGGATGGAGAAACAAAGACTACAGATGTAGAGAGA 375  
 407 ACATTGGAAGAACAGTAGAGGATGGAGAAACAAAGACTACAGATGTAGAGAGA 466  
 376 CCCTCTGAGAGAGTAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 435  
 467 GCCTCCACAGT 526  
 436 TGTAAACTTGTGATACCGGCA-----AAAAATTAAGTTGTGATCATTCAAGATGG 489

Db 527 GCAAAACATGGAACACCTTACCAATACATAATAGTCCATTACCAAGATGG 586  
 QY 490 CATTGCC 497  
 Db 587 GCATTGCC 594  
 RESULT 7  
 LOCUS AM495481/c  
 DEFINITION 499 bp mRNA linear EST 24-FEB-2000  
 UI-M-BH3-ay-g-11-0-UI-s1 NIH\_BMAP\_M.S4 Mus musculus cDNA clone  
 UI-M-BH3-ay-g-11-0-UI 3', mRNA sequence.  
 ACCESSION AM495481  
 VERSION AM495481.1 GI:7065762  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 499)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 COMMENT Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: MEST@emil.nih.gov  
 The sequence contained an oligo-dT track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. The sequence tag present in the cDNA between the NotI site  
 and the oligo-dT track served to identify it as a clone from the  
 normalized pineal glands library cDNA library Preparation: M.B.  
 Soares Lab Clone distribution: Researchers may obtain BMAP cDNA  
 clones from RESEARCH GENETICS. It should be noted that Bento Soares  
 is generating a small number of additional specialized  
 non-redundant arrays of BMAP cDNAs whose availability will be  
 considered under appropriate and limited collaborative arrangements  
 Seq primer: M13 Forward  
 POLYA=yes.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /strain="G57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UI-M-BH3-ay-g-11-0-UI"  
 /clone\_lib="NIH\_BMAP\_M.S4"  
 /dev\_stage="27-32 days"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site: 1; Not I; Site: 2; Eco RI; The  
 NIH\_BMAP\_M.S4 library is a subtracted library of a series,  
 ultimately derived from a mixture of individually tagged  
 normalized libraries from ten regions of the mouse brain  
 (cerebellum, brain stems, olfactory bulbs, hypothalamus,  
 cortex, amygdala, basal ganglia, pineal gland, striatum,  
 hippocampus) after a series of subtractions to reduce the  
 representation of cDNAs from which ESTs had already been  
 generated. The following serially subtracted libraries  
 were generated in this process: NIH\_BMAP\_M.S4,  
 NIH\_BMAP\_M.S3.3, NIH\_BMAP\_M.S3.2, NIH\_BMAP\_M.S3.1,  
 NIH\_BMAP\_M.S2, NIH\_BMAP\_M.S1. The subtracted library  
 cDNA inserts from NIH\_BMAP\_M.S3.3, NIH\_BMAP\_M.S3.2, and  
 NIH\_BMAP\_M.S3.1 clones from which 3' ESTs had been derived  
 was used as a driver in a hybridization with a pool of  
 the NIH\_BMAP\_M.S3.3, NIH\_BMAP\_M.S3.2, and NIH\_BMAP\_M.S3.1



Query Match 61.3% Score 320.8; DB 14; Length 673;  
Best Local Similarity 84.2% Pred. No. 6.2e-78;  
Matches 443; Conservative 0; Mismatches 27; Indels 56; Gaps 5;

QY	1	GGACCGGAGAGCGCTCTGCGGTGCTGAGTGTGATGCTCTTTCAGTTCTGATGTGTGGAGAC	60
Db	492	GGACCGGAGAGCGCTCTGCGGTGCTGAGTGTGATGCTCTTTCAGTTCTGATGTGTGGAGAC	433
QY	61	AGGGCGCTTTATTTTCACAAAGCCACAGAGATACGGCTCCAGCACTCGAGGGGCACTCAG	120
Db	432	AGGGG-TTTTATTTTCAGAAAGCCACAGAGATGTGGCTCCAGCACTCGAGGGGCGCTCAG	374
QY	121	ACAGCATCTGTGATGAGTGTGCTGCTCCGAGCTGTGATCTGAGAGAGCTGAGATGTAC	180
Db	373	ACAGCATCTGTGATGAGTGTGCTGCTCCGAGCTGTGATCTGAGAGAGCTGAGATGTAT	314
QY	181	TGTGACCCCTCAAGCCGGCAAGGCGAGCCGCTCCGTCGTCGCCACGCCACACCGAC	240
Db	313	TGCCACCCCTCAAGCCGTCGCCAAGTCAGCTGCTGCTGCTGCCACGCCACACCGAC	254
QY	241	ATGCCCAAGACTCAGAGAGTATCAGCCCTCCATCTCTCCAAACAAGAAATGAGTCTCAGAGG	300
Db	253	ATGCCCAAGACCCAG-----	239
QY	301	AGAAAGAAAGAGATACATTGGAAGAACACAGTAGAGGAGTGCAGAGAAACAAGAACTA	360
Db	238	-----AAGAAATACATTGTAAGAGACGCAAGTAGAGGAGTGCAGAGAAACAAGAACTA	186
QY	361	CAGGATGTAGAAACCCCTCTGAGGAGTGAAGAAGACAGCCACCGCAGAGACCTTTG	420
Db	185	CAGGATGTAGAAACCCCTCTGAGGAGTGAAGAGTACATGCCACCGCAGAGATCTTTG	126
QY	421	CTCTGCAC-AGTFACTG-TAAACATTGGAATACCGGCCCAAAATTAAGTTGATCAAT	478
Db	125	CTCTGCACGAGTACTCTGTTAACTTTGGAACACCTACCAAAAATTAAGTTGATCAAT	66
QY	479	TTCAAGAT-GGCATTTTCCCCCAATGAAATACAGAAATAAACATTC	523
Db	65	TTAAAGATGGGGCTTTCCTCCCAATGAAATACAGAAATAAACATTC	20

RESULT 10  
A1248089/c 575 bp mRNA linear EST 01-DEC-1998  
LOCUS A1248089  
DEFINITION q169f05.x1 Soares\_fetal\_liver\_spleen\_LINFS\_S1 Homo sapiens cDNA  
clone IMAGE:1849953 3' similar to gb:K57025\_fetal INSULIN-LIKE  
GROWTH FACTOR 1A PRECURSOR (HUMAN);, mRNA sequence.  
A1248089  
ACCESSION A1248089.1 GI:3843486  
VERSION EST.  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiindae; Homo.  
REFERENCE 1 (bases 1 to 575)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicap.  
TITLE National Cancer Institute, Cancer genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-f@mail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert length: 918 Std Error: 0.00  
Seq primer: -40up from Gibco  
High quality sequence stop: 380.  
Location/Qualifiers  
1. 575  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1849953"  
/clone\_1b="Soares\_fetal\_liver\_spleen\_LINFS\_S1"

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TITLE      Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
JOURNAL    Unpublished (1998)
COMMENT    Other_ESTs: TC50779
            Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-836-3529
            Fax: (301)-838-0208
            Email: nhlee@igf.org
            Seq primer: M13-21.
FEATURES   Location/Qualifiers
            source
              1..468
              /organism="Rattus sp."
              /db_xref="ATCC /Inhoest /2027570"

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/clone="RLIA07"
/clone_lib="Normalized rat liver, Bento Soares"
/notes="Organ: liver; Vector: pRT3pac; Site_1: Ecort;
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BASE COUNT	ORIGIN
85 a	115 c
119 g	149 t

Query Match	59.1%;	Score 309.2;	DB 9;	Length 468;
Best Local Similarity	81.8%;	Pred. No. 9e-75;		
Matches 383;	Conservative	0;	Mismatches 78;	Indels 7; Gaps

DY 63 GGGCTTTATTTCACAGCCCAAGGATACGGCTCCAGCAGTGGAGGGGCACCCTCAGAC 1  
||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||  
Db 468 GGCGTTTACTTCACAGGCCCAAGGCTATGGCTCCAGCATTCGGAGGGGCACCACAGAC 4

OY  
123 AGGCATCGTGAATGAGTCCTGCCGTCCGGAGCTTGATCTGAGGAGCCTGGAAATGTACTG 1

Nb  
408 GGGCATTTCTGGATTACACTGCTCCCCCCCCCCAACCCTGCAATCTATAATCTTAATCTAACCTAC 2

QY 183 TGCACCCCTCAAGCCGCGCAAGCGCAGCCCGCTCCGTCCTGCCAGCGCCACACCGACAT 2

243 GCCCAGACTCAGAGTATCAGCTCCATTACCAACAAGAAATGAACTCTCAGAGAG 3

D<sub>b</sub> 288 GCCCAGACTCAGAGATCCACGCCCTTATCGACACACAGAAAAAGAAAGCTGCAAGAG 2

Q<sub>Y</sub> 303 AAGGAAGGAGTACATTTTGAAGACACAAGTAGAGGAGTGCAGGAATAACAGACTACA 3

Accession	Sequence	Length
Ox	363 GGATGTAGGAAGACCCCTTCTGAGGATGTAAGGAAGGACAGGCCACCGACGAGGACCCCTTTGCT	4
Db	228 AAGGAAGGANGTACACTTGAGGACACACAGTAGAGGAAGTGCAGGAACACAGACCTACA	1

168 G A A T G T A G G A G A G C C T C C C G A G A C A G A A A T G C C A C G T C A C C G C A G A G A T C C T T T G C T 1

Db 108 GCTGACCACTGCAAAACATGGAAACACCCTGCCAATATCATATATGAGTTCAATGCC 41

47 ATTTCAGAGAT-GGCATTTCGCCCAATGAATACACAGTAATACATTCC 523  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
48 ATTTCAGAGATGGGCATTTCCTCAATGAATACACAGTAATACATTCC 1

RESULT 12  
AA542914/C

	496 bp	mRNA	linear	EST:19-AUG-1998
LOCUS	NM_047514			
DEFINITION	n198c10.s1 NC1_CGAP_P121 Homo sapiens CDNA clone IMAGE:984882 3'			
	similar to pX57025_rna1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR			
	(HUMAN); mRNA sequence			

ACCESSION	AA542914
VERSION	AA542914.1
KEYWORDS	GI:2291394
SEQUENCE	EST.
ANNOTATION	

ORGANISM      Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 498)  
 NCBI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-r@mail.nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CCAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnl.gov/bdrp/image/image.html  
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 High quality sequence stop: 412.  
 Location/Qualifiers  
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 1..498  
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 /clone="IMAGE:984882"  
 /clone\_lib="NCI-CCAP\_Pr21"  
 /sex="male"  
 /tissue\_type="normal prostate"  
 /lab\_host="DH10B"  
 /note="Organ: Prostate; Vector: pTR30-Pac (Pharmacia)  
 with a modified polylinker; 1st strand cDNA was prepared  
 from normal prostate bulk tissue, and was then primed with  
 a Not I - oligo(dT) primer. Double-stranded cDNA was  
 ligated to Eco RI adapters (Pharmacia), digested with Not  
 I and cloned into the Not I and Eco RI sites of the  
 modified pTR30 vector. Library is not normalized. Library  
 was constructed by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 105 a 135 c 125 g 135 t  
 ORIGIN  
 Query Match 58.3%; Score 305; DB 9; Length 498;  
 Best Local Similarity 83.5%; Pred. No. 1.3e-73;  
 Matches 440; Conservative 0; Mismatches 30; Indels 57; Gaps 6;  
 QY 1 GGACGGAGACGCTTCGCGTGC-TAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGA 59  
 Db 476 GGACGGAGACGCTTCGCGGCTTGAAGTGGATGCTCTTCAGTTCGTGTGGAGA 417  
 QY 60 CAGGCGCTTTATTTCAACAGCCACAGAGATACGGCTCCAGCTCGAGGGGCACTCA 119  
 Db 416 CAGGGGC-TTATTTCAACAGCCACAGAGATAGCTCCAGCTCGAGGGGCGCTCA 358  
 QY 120 GACAGCATGTGGATGAGTGTCTTCGCGAGCTGTATCTGAGAGAGGCTGGAGATGA 179  
 Db 357 GACAGCATGTGGATGAGTGTCTTCGCGAGCTGTATCTGAGAGAGGCTGGAGATGA 298  
 QY 180 CTGACACCCCTCAAGCCGCAAGAGCAGCCGCTCCGCTGCGGCAAGCCGCAACCGA 239  
 Db 297 TTGGGCAACCCCTCAAGCCGCAAGTCAAGTCAAGTCTGCTGCGGCAAGCCGCAACCGA 238  
 QY 240 CATGCCCAAGACTCAGAGTATCAGCTCCATCTACCAACAAAGAAATGAAGTCTCAGAG 299  
 Db 237 CATGCCCAAGACTCAGAGTATCAGCTCCATCTACCAACAAAGAAATGAAGTCTCAGAG 222  
 QY 300 GAGAGGAGAGAGATGATTTGAGAGACAGAGTAGAGGAGTGCAGAGAAACAGAACT 359  
 Db 221 -----AAGGAGAGTATGATTTGAGAGACAGAGTAGAGGAGTGCAGAGAAACAGAACT 170  
 QY 360 ACAGAGATGTAGAGAGCCCTTCTGAGAGAGTGAAGAGAGAGCCAGCCAGAGACCTTT 419  
 Db 169 ACAGAGATGTAGAGAGCCCTTCTGAGAGAGTGAAGAGAGTGAAGAGAGTGAAGAGTGA 110  
 QY 420 GCTGTGACG-AGTTACCTG-TAAACATTTGAGATACCGGCAAAATAAGTTGATGACA 477  
 Db 109 GCTGTGACGAGTTACTGTTAAAGCTTTGAGACACTACCAAAAATAAGTTGATGACA 50

QY 478 TTTCAGAGAT-GGCAATTTCCTCCCAATGAATACAGAGTAACATTC 523  
 Db 49 TTTCAGAGATGGCGCTTTCCTCCCAATGAATACAGAGTAACATTC 3  
 RESULT 13  
 A1604642  
 LOCUS  
 DEFINITION  
 882 bp mRNA linear EST 21-APR-1999  
 vnt3308.y1 Striatum mouse diaphragm (#937303) Mus musculus cDNA  
 clone IMAGE:1001007 5', similar to gb:U11568 INSULIN-LIKE GROWTH  
 FACTOR 1B PRECURSOR (HUMAN); gb:U04442 mouse mRNA for  
 preproinsulin-like growth factor 1B (MOUSE); mRNA sequence.  
 A1604642  
 A1604642.1 GI:4613809  
 EST.  
 house mouse.  
 SOURCE  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 882)  
 REFERENCE  
 AUTHORS  
 Maria M., Haller L., Kucaba T., Martin J., Beck C., Wylie T.,  
 Underwood K., Steptoe M., Theising B., Allen M., Bowers Y., Person  
 B., Swaller T., Gibbons M., Page D., Harvey N., Schurk R., Ritter  
 E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann R.,  
 Waterston R. and Wilson R.  
 The WashU-NCI Mouse EST Project 1999  
 JOURNAL  
 COMMENT  
 Unpublished (1999)  
 Contact: Maria M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 WCI:565223  
 This read is a RESEQUENCE of a previously sequenced mouse clone  
 This read has been verified (found to hit its original self in the  
 correct orientation)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 361.  
 Location/Qualifiers  
 source  
 1..882  
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 /db\_xref="taxon:10090"  
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 /tissue\_type="diaphragm"  
 /dev\_stage="adult"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /note="Organ: diaphragm; Vector: plasmid; SK: Site 1:  
 EcoRI; Site 2: XhoI; Cloned unidirectionally from mRNA  
 prepared from diaphragm muscle. Primer: Oligo dT. Average  
 insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor  
 sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5'  
 CTGAGCTTTTCTTTTCTTTT 3'."  
 BASE COUNT 236 a 226 c 183 g 223 t 14 others  
 ORIGIN  
 Query Match 57.2%; Score 299; DB 9; Length 882;  
 Best Local Similarity 77.2%; Pred. No. 7.3e-72;  
 Matches 393; Conservative 0; Mismatches 109; Indels 7; Gaps 3;  
 QY 1 GGACGGAGACGCTTCGCGTGC-TAGCTGGTGGATGCTCTTCAGTTCGTGTGGAGA 60  
 Db 377 GGACGGAGACGCTTCGCGGCTTGAAGTGGATGCTCTTCAGTTCGTGTGGAGA 436  
 QY 61 AGGCGCTTTATTTCAACAGCCACAGAGATACGCTCCAGAGTGGAGGCGACTCAG 120  
 Db 437 AGGCGCTTTTACTCTCAACAGCCACAGAGCTATGCTCCAGATTTGAGGCGACTCAG 496  
 QY 121 ACAGCATGTGATGAGTGTCTTCGCGAGCTGTGATCTGAGAGGCTGAGATGTAC 180

RESULT 14	BQ200567/c	LOCUS	DEFINITION	ACCESSION
BQ200567	653 bp.	MRNA	linear	EST 02-MAY-2002
UI-R-D21-cme-a-18-0-UI	si	UI-R-D21	Rattus norvegicus	CDNA clone
UI-R-D21-cme-a-18-0-UI	3'			RNA sequence.
BQ200567				

	653 bp	RNA	linear	EST 02-MAY-2002
BQ200567				
UI-R-D21-cme-a-18-0-UI.s1			UI-R-D21	Rattus norvegicus cdna clone
UI-R-D21-cme-a-18-0-UI.3				mRNA sequence.
BQ200567				
BQ200567.1	GI:20417032			
EST.				

Genome Res. 6 (9), 791-806 (1996)  
070444477

Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
National Institute of Health

451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565

Email: [msoares@blue.weeg.uiowa.edu](mailto:msoares@blue.weeg.uiowa.edu)

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to verify it as a clone from the normalized cartilaginous tumor library cDNA library. Proportion-

M.B. Soares Lab clone distribution: clones will be available through Research Corvicia (<http://www.researchcorvicia.com>)

through research genetics ([www.resgen.com](http://www.resgen.com)) The following repetitive elements were found in this cDNA sequence: 1-43,

```
>ai_rich#Low_complexity 118-164, >POLY_A#Simple_repeat
Seq primer: M13 Forward
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POLYA=Yes.

FEATURES	Location/Qualifiers
source	1. .653

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1. .653
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-D21-cne-a-18-0-UI"
/clone_1lb="UI-R-D21"
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/tissue.type="Chondrosarcoma"
/dev.stage="37 days"
/lab.host="DH10B (Life Technologies)"
/note="Organ: Spine; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI;
UI-R-D21 is a normalized cDNA library containing the
following tissue(s): Swarm Rat Chondrosarcoma. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73D-Pac vector. The oligonucleotide used to prime
the synthesis of first strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CATTCTGTA. The Rat cartilaginous tumor tissue was
provided by Dr Jeff Stevens at the University of Iowa.
TAG_Lib=ui-R-D21
TAG_TISSUE=cartilaginous tumor
TAG_SEQ=CATTCTGTA"
134 a 137 c 137 g 245 t

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Query Match	56.7%	Score 296.4;	DB 14;	Length 653;
Best Local Similarity	81.9%	Pred. No. 3.5e-71;		
Matches 380; Conservative	0;	Mismatches 76;	Indels 8;	Gaps 3

67 TTTTATTTCACAGAGCCACAGATACGGCTCCAGCAGTCCGAGGGCACCTCAGACAGGC 126

Db 653 TTTTACTTCACACAGCCACAGGCTATGGCTCCAGCATTCGAGGGCACCACAGACGGGC 594

QY 127 ATCGTGATGAGTCTGCTTCCTCCGGAAGCTGTGATCTGAGGAGGCTGAGATGTAATCTGCA 185

[illegible][illegible]

10 / ccccttcaaaccccgcaaaagagccccgcgtccgttccgttgccacagccacacccgacatgcc 246

Db 534 CCGCTGAAGCCTACAAAGTCAAGCTGTTCCATCCGGGCCCCAGCGCCACACTGACATGCC 475

247 AAGACTCAGAAGTATCAGCCTCCATCTACCAACAGAAGAAATGAAGTCTCAGAGGAGAAG 306

Db 474 AAGACTCAGAAGTCCACGCCCTATCGACACACAGAAAGGAGCTGCAAAAGGAGAAG 415

307 AAAGGAGTACATTTGAGCAACACCAAGTAGAGGGAGTGCAGGAACAGAAGACTACAGGAT 366

Db 414 A A A G A G T A C A C T T G A G A G A C A C A G T A G A G A A G T G C A G G A A A C A C A C C T T A C A G A A T 355

367 GTAGNAGACCCCTTCTGAGAGTGAAGAAGACACAGGCCACCGCAGGACCCCTTGTCTGAC 426

Dpb  
354 GTTGGAGGACCTCCCGAGGAACACGAAAAATGCCGCCTCACCACCAAGCACGCCCCGTCCTTCCTCCGTTT 305

[illegible][illegible]

234 GAGCAACCTGCAAAACATGGAGACACACCTGCAATATCATATATGAGTTCATATACCATT 235

481 CAAGAT-GGCATTTCCCCCATGAAATACCAAGTAAACATTC 523

Db 234 CAGAGATGGGCATTTCCTCAATGAAATACACAGTAACATTTC 191

DEPT. 15

RESOLU 13  
AA913900/c  
20010000

LOCUS	527 bp	mRNA	linear	EST 24-SEP-1998
DEFINITION	0135g05.s2 Soares.NFL_T_GBC_S1 Homo sapiens CDNA clone			

IMAGE:1525496 3' similar to gb:X57025\_rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN)?: mRNA sequence.

ACCESSION	AA913900
VERSION	AA913900 1
	GI:3053292

KEYWORDS	
EST.	
SOURCE	
human	

ORGANISM	Source
Homo sapiens	human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

